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Die folgenden Angaben sind den vom Anmelder eingereichten Unterlagen entnommen

(54) Bezeichnung: **Humane Nukleinsäuresequenzen aus Bronchialkarzinomen**

(57) Zusammenfassung: Die Erfindung betrifft neue humane Nukleinsäuresequenzen aus Bronchialkarzinomen, hierdurch codierte Proteine bzw. Peptide sowie deren Verwendungen im Zusammenhang mit der Diagnose und/oder Behandlung von Bronchialkrebs.

Beschreibung

Gebiet der Erfindung

[0001] Die Erfindung betrifft neue humane Nukleinsäuresequenzen aus Bronchialkarzinomen sowie hierdurch codierte Proteine bzw. Peptide, die Verwendung von hieraus abgeleiteten Sequenzen zum Screenen nach daran bindenden Substanzen, sowie die Verwendung von an solche Nukleinsäuresequenzen und Proteine bzw. Peptide bindenden Substanzen zur Diagnose und/oder Behandlung von Tumorerkrankungen, insbesondere Bronchialkrebs.

Stand der Technik

[0002] Krebs, insbesondere Lungenkrebs, ist eine mit zunehmendem Alter und im Zusammenhang mit Nikotinkonsum mit beachtlicher Inzidenz auftretende Erkrankung. Das Bronchialkarzinom ist derzeit die häufigste Todesursache aller Krebskranken Männer und Frauen in Nordamerika und Europa. Die Fünf-Jahres-Überlebensrate aller Bronchialtumorpatienten liegt bei nur 13%. Lediglich die Patienten mit noch lokal begrenzten Lungentumorerkrankungen zeigen eine Fünf-Jahres-Überlebensrate von 46%. Allerdings werden nur 16% der Bronchialkarzinome in diesem frühen Tumorstadium diagnostiziert.

[0003] Bislang wird die Lungentumorerkrankung im wesentlichen durch eine histopathologische Diagnose manifestiert. Die anschließende Therapie richtet sich nach dem Tumorstadium, der Lokalisation und der Ausbreitung des Tumors sowie nach der körperlichen Verfassung des Patienten. Die Therapie der Wahl bei einem nicht-kleinzelligen Lungenkarzinom der frühen Stadien besteht in der potentiell kurativen Operation. Dies bezieht sich auf die Stadien I und II und in Verbindung mit postoperativer Strahlentherapie auch auf das Stadium IIIA. Eine primäre Operation ist jedoch nur bei 25–30% aller Patienten möglich. Im Stadium IIIA mit Lymphknotenmetastasen sowie im Stadium IIIB dominiert die Radiotherapie. In den letzten Jahren tritt bei diesen Patienten der multimodale Therapieansatz mehr und mehr in den Vordergrund. Bei gering ausgeprägtem und vermutlich technisch vollständig resektablem N2 konkurrieren primäre Operation und Nachbestrahlung mit einem neoadjuvanten Therapieansatz und anschließender Operation. Das neoadjuvante Konzept mit initialer Chemotherapie oder Chemoradiotherapie sowie anschließender Operation hat sich in der fortgeschrittenen N2 Situation bzw. im Stadium IIIB weitgehend durchgesetzt. Im disseminierten Stadium IV dominiert die Chemotherapie als palliative Behandlung, zum Teil ergänzt durch die Radiotherapie.

[0004] Der operative Eingriff mit einer Teilentfernung einzelner befallener Lungenlappen und anschließender Chemo- und/oder Radiotherapie hat verschiedene nachteilige Effekte auf die Physis und Psyche der betroffenen Patienten, was in der Regel zu einer starken Einschränkung der Lebensqualität führt. Daher ist eine verbesserte Diagnose und Behandlung von Bronchialtumorpatienten, insbesondere mit einer Verbesserung der Überlebenszeiten und Lebensqualität, in einem hohem Maße wünschenswert.

Aufgabenstellung

Technisches Problem der Erfindung

[0005] Der Erfindung liegt daher das technische Problem zugrunde, pharmazeutische Zusammensetzungen zur Diagnose und/oder zur Behandlung von Bronchialkrebs-erkrankungen anzugeben sowie Mittel zu deren Findung.

[0006] Grundzüge der Erfindung sowie bevorzugte Ausführungsbeispiele.

[0007] Zur Lösung dieses technischen Problems lehrt die Erfindung zunächst eine Nukleinsäure enthaltend oder bestehend aus einer Nukleinsäuresequenz gemäß einer der Sequenzen Seq.-ID 1 bis 489 sowie ein Peptid oder Protein enthaltend eine Aminosäurensequenz codiert durch eine der Nukleinsäuresequenzen Seq.-ID 1 bis 489 oder bestehend hieraus oder enthaltend eine Aminosäurensequenz gemäß einer der Sequenzen 499 bis 978 oder bestehend hieraus. Erfindungsgemäße Nukleinsäuren oder Proteine bzw. Peptide lassen sich mit den üblichen molekularbiologischen Methoden herstellen.

[0008] Die Erfindung betrifft weiterhin verschiedene Verwendungen der neuen Nukleinsäuren bzw. Peptide oder Protein, ebenso wie (gleiche) Verwendungen bereits bekannter Nukleinsäuren. Diese sind:

i) Verwendung einer erfindungsgemäßen Nukleinsäure und/oder eines erfindungsgemäßen Peptids oder Proteins, zur Detektion von Bronchialkrebs oder zur Detektion eines Risikos der Erkrankung an Bronchial-

krebs, wobei eine Lungen- bzw. Bronchial-Gewebeprobe auf Übertranskription der Nukleinsäure oder auf Überexpression des Proteins untersucht wird. Dabei kann eine an die Nukleinsäure oder eine an das Protein oder Peptid bindende Detektorsubstanz, vorzugsweise enthaltend eine Reportergruppe, verwendet werden, wobei Bindung besagter Nukleinsäure und/oder besagten Proteins oder Peptids an die Detektorsubstanz halbquantitativ oder quantitativ detektiert wird. Auch kann das Expressionsniveau durch Amplifikation, beispielsweise quantitative PCR, gemessen werden.

ii) Verwendung einer erfindungsgemäßen Nukleinsäure oder eines erfindungsgemäßen Proteins oder Peptids zum Screenen nach daran bindenden Substanzen, insbesondere prospektiven Wirkstoffen zur Inhibierung von besagter Nukleinsäure oder besagtem Protein oder Peptid, oder prospektiven Detektorsubstanzen, wobei eine prospektive Substanz oder eine Mischung solcher prospektiver Substanzen mit besagter Nukleinsäure oder besagtem Protein oder Peptid kontaktiert wird, wobei mit einem Bindungsassay Bindungsereignisse festgestellt werden, und wobei eine bindende prospektive Substanz, ggf. nach Dekonvolution, selektiert wird.

iii) Verwendung einer eine erfindungsgemäße Nukleinsäure oder ein erfindungsgemäßes Peptid bzw. Protein inhibierenden oder daran bindenden Substanz, insbesondere identifiziert mit dem erfindungsgemäßen Screening Verfahren, zur Herstellung einer pharmazeutischen Zusammensetzung zur Diagnose und/oder Behandlung von Bronchialkrebs.

[0009] Eine im Rahmen der Erfindung eingesetzte Substanz kann ausgewählt sein aus der Gruppe bestehend aus:

a) Antisense-Oligonukleotide, siRNA, und Ribozyme gegen eine Nukleinsäure nach Anspruch 1,

b) an ein Peptid oder Protein nach Anspruch 2 bindendes, insbesondere nach Anspruch 5 identifiziertes, organisches Molekül mit einem Molekulargewicht unterhalb 5000, vorzugsweise unterhalb 1000, höchstvorzugsweise unterhalb 300,

c) Aptamer gegen ein Protein oder Peptid nach Anspruch 2, insbesondere identifiziert nach Anspruch 5,

d) (monoklonaler) Antikörper, insbesondere humaner oder humanisierter Antikörper gegen ein Protein oder Peptid nach Anspruch 2,

e) anti-idiotypischer nicht-humaner (monoklonale) Antikörper, generiert mittels eines Antikörpers der Untergruppe d), und

f) vorstehende Substanzen derivatisiert mit einer Reportergruppe, einem Zelltoxin, einer immunstimulierenden Komponente und/oder einem Radioisotop.

[0010] Im Falle a) kann als Ribozyme beispielsweise ein Hammerhead Ribozym eingesetzt werden. Die Ribozym-Schnittstelle wird mit der Maßgabe ausgewählt, dass durch die Aktivität des Ribozymes die Expression des Proteins entweder unterbunden wird, oder eine inaktive Form bzw. ein inaktives Fragment des Proteins exprimiert wird. Beides läßt sich beispielsweise dadurch ermitteln, dass in einem Zellsystem, in welchem ein erfindungsgemäßes Protein auf definiertem Niveau exprimiert wird, dieses Zellsystem mit einem oder mehreren für definierte Schnittstellen modelliertes Ribozym kontaktiert wird und das Expressionsniveau bestimmt bzw. die biologische Aktivität des exprimierten Proteins. Dies wird dann verglichen mit einer Negativprobe bzw. den Ergebnissen ohne Kontaktierung und Ribozyme werden selektiert, die zu niedrigerer Expression oder Aktivität führen. Entsprechend kann im Falle der siRNA oder der antisense Nukleinsäuren vorgegangen werden. Im Falle a) sind alle Sequenzen brauchbar.

[0011] Im Falle b) können chemische Stoffbibliotheken eingesetzt werden, um nach bindenden Substanzen zu screenen. Eine Validierung bindender Substanzen für therapeutische Zwecke kann durch Bestimmung der biologischen Aktivität des Proteins in einem Zellsystem mit und ohne Kontaktierung und Vergleich der erhaltenen Ergebnisse erfolgen. Für therapeutische Zwecke ausgewählt werden dann solche Stoffe, die zu einer reduzierten biologischen Aktivität führen. Es ist auch möglich, dass im Rahmen eines erfindungsgemäßen Screening Verfahren an Stelle der Bindung die biologische Aktivität bestimmt wird; dann ist eine Validierung im vorstehenden Sinne zugleich mit dem Screening erfolgt. Biologische Aktivität läßt sich beispielsweise dadurch bestimmen, dass natürliche Assoziationspartner des Proteins bestimmt und deren Vorkommen und Form (z.B. Monomer/Dimer/Heterodimer) untersucht werden. Es lassen sich auch weiter downstream in einer Stoffwechselkaskade entstehende Substanzen als Indikator verwenden; diese lassen sich beispielsweise dadurch identifizieren, dass zuvor Zellkomponenten analysiert werden für die das Protein exprimierende Zelle und ein Vergleich durchgeführt wird mit gleichen Zellen, in welchen jedoch die Expression gentechnisch deletiert ist. Im Einzelnen ist im Falle (b) folgendes anzumerken. Insbesondere ausgehend von den Nukleinsäuresequenzen 3; 6; 8; 9; 13; 15; 19; 20; 21; 23; 26; 28; 29; 30; 31; 32; 35; 37; 41; 46; 50; 52; 53; 55; 57; 58; 60; 62; 66; 68; 73; 77; 78; 79; 80; 81; 83; 87; 89; 92; 96; 99; 102; 112; 112.2; 112.3; 112.4; 112.5; 112.6; 124; 125; 129; 131; 135; 138; 139; 140; 142; 144; 146; 149; 154; 157; 160; 163; 165; 167; 168; 169; 170; 171; 172; 173; 174; 177; 178; 180; 181; 182; 183; 188; 189; 190; 191; 192; 193; 194; 195; 197; 198; 199; 201; 203; 206; 207; 211; 212;

213; 214; 215; 216; 218; 220; 223; 224; 230; 232; 233; 234; 235; 238; 239; 241; 242; 243; 244; 247; 249; 250; 254; 259; 262; 263; 266; 267; 268; 269; 274; 278; 280; 282; 283; 284; 286; 287; 288; 290; 293; 296; 298; 299; 308; 310; 312; 315; 316; 317; 320; 320.2; 322; 323; 324; 326; 328; 334; 338; 339; 341; 342; 343; 344; 345; 346; 348; 354; 356; 357; 359; 360; 367; 369; 370; 372; 376; 379; 380; 394; 395; 396; 397; 399; 402; 412; 417; 421; 425; 428; 429; 431; 432; 439; 448; 452; 456; 461; 462; 463; 468; 470; 471; 472; 473; 474; 475; 476; 478; 482; 484; 487; 489 können Mimikry-Verbindungen abgeleitet werden, welche in der Lage sind, spezifisch das funktionell aktive Zentrum der Enzymdomänen-enthaltenden Proteine zu binden und in ihrer biologischen Aktivität zu inhibieren. Sollte eine Mimikry-Verbindung in der Lage sein, spezifisch die Peptide 492; 495; 497; 498; 502; 504; 508; 509; 510; 512; 515; 517; 518; 519; 520; 521; 524; 526; 530; 535; 539; 541; 542; 544; 546; 547; 549; 551; 555; 557; 562; 566; 567; 568; 569; 570; 572; 576; 578; 581; 585; 588; 591; 601; 601.2; 601.3; 601.4; 601.5; 601.6; 613; 614; 618; 620; 624; 627; 628; 629; 631; 633; 635; 638; 643; 646; 649; 652; 654; 656; 657; 658; 659; 660; 661; 662; 663; 666; 667; 669; 670; 671; 672; 677; 678; 679; 680; 681; 682; 683; 684; 686; 687; 688; 690; 692; 695; 696; 700; 701; 702; 703; 704; 705; 707; 709; 712; 713; 719; 721; 722; 723; 724; 727; 728; 729; 730; 731; 732; 733; 736; 738; 739; 743; 748; 751; 752; 755; 756; 757; 758; 763; 767; 769; 771; 772; 773; 775; 776; 777; 779; 782; 785; 787; 788; 797; 799; 801; 804; 805; 806; 809; 809.2; 811; 812; 813; 815; 817; 823; 827; 828; 830; 831; 832; 833; 834; 835; 837; 843; 845; 846; 848; 849; 856; 858; 859; 861; 865; 868; 869; 883; 884; 885; 886; 888; 891; 901; 906; 910; 914; 917; 918; 920; 921; 928; 937; 941; 945; 950; 951; 952; 957; 959; 960; 961; 962; 963; 964; 965; 967; 971; 973; 976; 978 zu binden, ohne es in ihrer biologischen Funktion zu inhibieren, kann es trotzdem zur Lösung des technischen und medizinischen Problems beitragen. Es kann als guter Binder mit einem Zelltoxin derivatisiert werden, um somit in einem Targeting Approach die Zielzellen abzutöten. Ein solches Zelltoxin kann ein klassisches Chemotherapeutikum aber auch ein Radioisotop sein. Ebenfalls können solche Peptid-spezifische Mimikry-Verbindungen, mit einer Reportergruppe derivatisiert, als Verbindung in der Tumordiagnostik verwendet werden.

[0012] Geeignete Aptamere (c) lassen sich unschwer beispielsweise mittels des wohlbekannten SELEX Verfahren identifizieren, wobei das erfindungsgemäße Protein als Target eingesetzt wird. Einsetzbar sind alle Sequenzen.

[0013] Antikörper (d), insbesondere monoklonale Antikörper, können in üblicher Weise durch Immunisierung eines nicht-menschlichen Säugetiers mit einem erfindungsgemäßen Protein, einer erfindungsgemäßen Nukleinsäure (z.B. cDNA), einer ein erfindungsgemäßes Protein konstitutiv exprimierenden Zelle (Krebszelle oder beispielsweise mit einer erfindungsgemäßen Nukleinsäure transfizierte Zelle, wie COS oder NIH3T3), oder mittels recombinant hergestelltem erfindungsgemäßem Protein oder Peptid, beispielsweise in E.coli oder Eukaryontenzellen (z.B. Insektenzellen) exprimiert, erhalten werden. Monoklonale Antikörper sind durch übliche Selektion und Etabilierung von Hybridomzellen erhältlich. Auch kann die Phage Display Technologie zur Generierung der Antikörper eingesetzt werden. Für den Fall (d) ist ergänzend folgendes anzumerken. Ausgehend insbesondere von extrazellulär exponierten Peptiden oder

[0014] Proteinen 490; 491; 493; 494; 496; 499; 500; 501; 502; 503; 505; 506; 507; 511; 513; 514; 516; 520; 522; 523; 525; 527; 528; 529; 530; 531; 532; 533; 534; 536; 537; 538; 540; 543; 545; 548; 550; 551; 552; 553; 554; 556; 557; 558; 559; 560; 561; 563; 564; 565; 568; 571; 573; 574; 575; 577; 578; 579; 580; 582; 583; 584; 585; 586; 587; 589; 590; 592; 593; 594; 595; 596; 597; 598; 599; 600; 602; 603; 604; 605; 606; 607; 608; 609; 610; 611; 612; 615; 616; 617; 619; 621; 622; 623; 625; 626; 630; 631; 632; 634; 636; 637; 638; 639; 640; 641; 642; 644; 645; 647; 648; 650; 651; 653; 655; 658; 664; 665; 668; 669; 670; 673; 674; 675; 676; 678; 682; 683; 685; 689; 691; 693; 694; 697; 698; 699; 706; 707; 708; 7.10; 711; 712; 714; 715; 716; 717; 718; 720; 721; 725; 726; 734; 735; 737; 740; 741; 742; 744; 745; 746; 747; 749; 750; 753; 754; 757; 758; 759; 760; 761; 762; 764; 765; 766; 768; 770; 772; 774; 778; 780; 781; 782; 783; 784; 786; 788; 789; 790; 791; 792; 793; 794; 795; 796; 798; 800; 802; 803; 804; 805; 807; 808; 810; 813; 814; 816; 817; 818; 819; 820; 821; 822; 823; 824; 825; 826; 828; 829; 830; 836; 838; 839; 840; 841; 842; 843; 844; 847; 850; 851; 852; 853; 854; 855; 856; 857; 860; 862; 863; 864; 866; 867; 870; 871; 872; 873; 874; 875; 876; 877; 878; 879; 880; 881; 882; 884; 886; 887; 889; 890; 891; 892; 893; 894; 895; 896; 897; 898; 899; 900; 902; 903; 904; 905; 907; 908; 909; 910; 911; 912; 913; 914; 915; 916; 919; 922; 923; 924; 925; 926; 927; 929; 930; 931; 932; 933; 934; 935; 936; 937; 938; 939; 940; 942; 943; 944; 946; 947; 948; 949; 953; 954; 955; 956; 958; 959; 961; 962; 963; 966; 967; 968; 969; 970; 972; 974; 975; 977 kann ein Antikörper in humaner und/oder humanisierter Form abgeleitet werden, welcher in der Lage ist, spezifisch das funktionell aktive Zentrum der Proteine zu binden und in deren biologischer Aktivität zu inhibieren. Ebenfalls kann ein solcher Peptide-spezifischer Antikörper, mit einer Reportergruppe derivatisiert, als Verbindung in der Tumordiagnostik verwendet werden.

[0015] Im Falle der anti-idiotypischen Antikörper (e) sind diese dadurch erzeugbar, dass mittels eines erfindungsgemäßen Antikörpers, welcher nicht notwendigerweise die biologische Aktivität des erfindungsgemäßen

Proteins beeinflussen muss, in einem nicht-menschliche Säugetier ein zweiter anti-idiotypischer (monoklonaler) Antikörper generiert wird. Dieser anti-idiotypische Antikörper täuscht dann bei Applikation in humane Zellen dem humanen Immunsystem ein Bild des Zielmoleküls vor und wird aufgrund seiner nicht-humanisierten Form als körperfremdes Epitop erkannt. Der Mensch bildet folglich natürlicherweise Antikörper gegen den anti-idiotypischen Antikörper und somit auch gegen das Protein bzw. gegen das Protein exprimierende Zellen. Diese Variante der Erfindung ist ausschließlich für therapeutische Zwecke verwendbar. Ausgehend von Peptid- bzw. Proteinsequenzen 490; 491; 493; 494; 496; 499; 500; 501; 502; 503; 505; 506; 507; 511; 513; 514; 516; 520; 522; 523; 525; 527; 528; 529; 530; 531; 532; 533; 534; 536; 537; 538; 540; 543; 545; 548; 550; 551; 552; 553; 554; 556; 557; 558; 559; 560; 561; 563; 564; 565; 568; 571; 573; 574; 575; 577; 578; 579; 580; 582; 583; 584; 585; 586; 587; 589; 590; 592; 593; 594; 595; 596; 597; 598; 599; 600; 602; 603; 604; 605; 606; 607; 608; 609; 610; 611; 612; 615; 616; 617; 619; 621; 622; 623; 625; 626; 630; 631; 632; 634; 636; 637; 638; 639; 640; 641; 642; 644; 645; 647; 648; 650; 651; 653; 655; 658; 664; 665; 668; 669; 670; 673; 674; 675; 676; 678; 682; 683; 685; 689; 691; 693; 694; 697; 698; 699; 706; 707; 708; 710; 711; 712; 714; 715; 716; 717; 718; 720; 721; 725; 726; 734; 735; 737; 740; 741; 742; 744; 745; 746; 747; 749; 750; 753; 754; 757; 758; 759; 760; 761; 762; 764; 765; 766; 768; 770; 772; 774; 778; 780; 781; 782; 783; 784; 786; 788; 789; 790; 791; 792; 793; 794; 795; 796; 798; 800; 802; 803; 804; 805; 807; 808; 810; 813; 814; 816; 817; 818; 819; 820; 821; 822; 823; 824; 825; 826; 828; 829; 830; 836; 838; 839; 840; 841; 842; 843; 844; 847; 850; 851; 852; 853; 854; 855; 856; 857; 860; 862; 863; 864; 866; 867; 870; 871; 872; 873; 874; 875; 876; 877; 878; 879; 880; 881; 882; 884; 886; 887; 889; 890; 891; 892; 893; 894; 895; 896; 897; 898; 899; 900; 902; 903; 904; 905; 907; 908; 909; 910; 911; 912; 913; 914; 915; 916; 919; 922; 923; 924; 925; 926; 927; 929; 930; 931; 932; 933; 934; 935; 936; 937; 938; 939; 940; 942; 943; 944; 946; 947; 948; 949; 953; 954; 955; 956; 958; 959; 961; 962; 963; 966; 967; 968; 969; 970; 972; 974; 975; 977 können monoklonale Maus/Ratten Antikörper abgeleitet werden. Die monoklonalen Antikörper Ab1 müssen nicht notwendiger Weise in der Lage sein, spezifisch das funktionell aktive Zentrum der Proteine zu binden und in deren biologischer Aktivität zu inhibieren. Die monoklonalen Antikörper Ab1 werden im zweiten Schritt verwendet, um zweite anti-idiotypische maus-monoklonale Antikörper aAB1 zu generieren. Die monoklonalen aAB1 stellen die Verbindung zur Lösung des technischen und medizinischen Problems dar, in dem diese dem humanen Immunsystem ein Image des Antigens "vertäuscht" und durch seine nicht-humanisierte Form als körperfremdes Epitop erkannt wird. Der humane Körper bildet zwangsläufig eigene Antikörper gegen aAB1 und somit gegen die das Zielprotein exprimierenden Tumorzellen. Während sich die aAB1 Antikörper ausschliesslich zur Behandlung der Tumorerkrankung eignen, sind die Ab1 Antikörper ausschliesslich für die diagnostische Problemlösung zu verwenden.

[0016] Im Falle f) können ausgehend von den Nukleinsäuresequenzen 1 bis 489 und/oder den Aminosäuresequenzen 490 bis 978 Antikörper und/oder Mimikry-Verbindungen mit hoher spezifischen Bindungsaktivität isoliert werden. Solche Substanzen werden dann in einem zweiten Schritt mit Zelltoxinen und/oder Radioisotopen derivatisiert und zum Targeting der Tumorzellen eingesetzt.

[0017] Die Erfindung betrifft des weiteren ein Verfahren zur Diagnose einer Bronchialkxebserkrankung, wobei eine erfindungsgemäße pharmazeutische Zusammensetzung in der Ausführungsform mit einer Reportergruppe in zu untersuchendes Gewebe in vivo oder in vitro appliziert wird, wobei das zu untersuchende Gewebe dann einer Detektionsverfahrenstufe unterworfen wird, welche sensitiv für die Reportergruppe ist, und wobei im Fall der Detektion eines definierten Mindestwertes der Reportergruppe im Gewebe das Gewebe als Tumorzellen enthaltend qualifiziert wird, sowie ein Verfahren zur Behandlung einer Bronchialkrebs-erkrankung, wobei eine erfindungsgemäße pharmazeutische Zusammensetzung in einer physiologisch wirksamen Dosis einem Patienten dargereicht wird.

[0018] Die Erfindung beruht auf der Erkenntnis, daß erfindungsgemäße Gene bzw. Genprodukte differentiell in Bronchialtumorgewebe exprimiert werden, i.e. in Bronchialtumorgewebe ist die Expression höher oder niedriger, insbesondere höher, verglichen mit normalen Zellen gleichen Gewebes. Dies erlaubt es einerseits, insbesondere diese neuen Gene bzw. Genprodukte als Marker zur Identifizierung von Tumorzellen im Bronchialgewebe zu nutzen. Dabei kann die Untersuchung auf Marker in Proben von Blutserum oder Sputum erfolgen, was insbesondere im Bereich der Vorsorgeuntersuchung bzw. Frühdiagnostik vorteilhaft ist. Auf der anderen Seite bietet die Inhibierung der Gene bzw. Genprodukte, insbesondere auch bei lokaler Applikation, die Möglichkeit, in die Bronchialtumor-spezifischen Genprodukt-Assoziationen mit anderen Prozessen in den Tumorzellen einzugreifen und somit letztendlich den tumorzellenspezifisch veränderten Stoffwechsel zu stören und zu einem Absterben oder zumindest einer Wachstumshemmung der Bronchialtumorzellen beizutragen.

[0019] Im Rahmen der Erfindung kann es sich empfehlen, im Vorfeld einer Behandlung mit einer erfindungsgemäßen pharmazeutischen Zusammensetzung eine Probe aus einem Gewebe, welches als Tumorgewebe mit anderen Methoden identifiziert ist, zu entnehmen und die Gewebeprobe auf Expression bzw. Überexpres-

sion des erfindungsgemäßen Gens bzw. Genproduktes zu untersuchen. Alternativ kann mit einer erfindungsgemäßen Detektorsubstanz zur Diagnose in vivo auf Abhängigkeit von dem Gen bzw. Genprodukt getestet werden. Wird eine Expression bzw. Überexpression des Gens bzw. Genproduktes gegenüber Normalgewebe gleichen Typs festgestellt, so ist die Anwendung der erfindungsgemäßen pharmazeutischen Zusammensetzung indiziert.

[0020] Handelt es sich bei dem Tumor um einem Typus, bei welchem Tumorzellen ein erfindungsgemäßes Gen exprimieren, Normalzellen gleichen Gewebetyps jedoch nicht oder nur schwach, so ist es besonders bevorzugt, wenn die an das Gen bzw. das Genprodukt bindende Substanz zusätzlich eine zytotoxische und/oder immunstimulierende Komponente trägt. Dies führt dann letztendlich dazu, dass praktisch ausschließlich Tumorzellen getötet werden, sei es durch die Zytotoxizität, sei es durch Angriff durch das stimulierte Immunsystem, während Normalzellen in dem Gewebe praktisch vollständig erhalten bleiben. In dieser Ausführungsform braucht die bindende Substanz selbst nicht inhibierend auf das Gen bzw. Genprodukt zu wirken, da die bindende Substanz dann lediglich als Marker funktionieren muß, welcher die Komponenten zu Ziel-Tumorzellen trägt. Im Falle des Einsatzes einer zytotoxischen und/oder immunstimulierenden Komponente kann es sich besonders empfehlen, wenn die pharmazeutische Zusammensetzung zur lokalen Applikation in Tumorzellen enthaltendem Gewebe hergerichtet ist, beispielsweise zur Injektion.

[0021] Sofern im Rahmen der Beschreibung offenbarte und/oder beanspruchte Sequenzen per se vorbekannt sind oder Teile vorbekannter Sequenzen sind, sind die offenbarten Sequenzen, soweit sie mit vorbekannten Sequenzen übereinstimmen, insofern Gegenstand der Erfindung, als dass sie lediglich gemäß den beschriebenen Verwendungen eingesetzt werden. Offenbarte und/oder beanspruchte Sequenzen, welche Teile von vorbekannten Sequenzen sind, können mittels eines Disclaimers oder mehrerer Disclaimer in Ansprüchen so abgegrenzt werden, dass die vorbekannten Sequenzen nicht mit umfasst sind.

[0022] Die Nukleinsäurensequenzen 1 bis 171 sowie die Peptidsequenzen 490 bis 660 sind insbesondere geeignet im Falle von Adenokarzinomen. Die Nukleinsäuresequenzen 172 bis 290 und die Peptidsequenzen 661 bis 779 sind insbesondere geeignet im Falle von Adenokarzinomen und Plattenepithelkarzinomen bzw. den nicht-kleinzelligen Bronchialkarzinomen. Die Nukleinsäuresequenzen 291 bis 489 sowie die Peptidsequenzen 780 bis 978 sind insbesondere geeignet im Falle von Plattenepithelkarzinomen.

Definitionen.

[0023] Im Rahmen dieser Beschreibung umfasst eine Sequenz alle humanen Isoformen, Splice Varianten und regulatorische RNA, bekannt oder neu, auf Nukleinsäuren- oder Aminosäurenbasis, verwendet. Mit diesen Begriffen mit umfaßt sind auch die ggf. im Rahmen dieser Beschreibung offenbarten kurzen Sequenzen, welche aus den verschiedenen Varianten stammen, beispielsweise Immunisierungssequenzen. Weiterhin, mit umfaßt sind auch Homologe, wobei die Homologie zumindest 80%, vorzugsweise mehr als 90%, höchstvorzugsweise mehr als 95%, beträgt (berechnet mit dem Programm MEGALIGN, DNASTAR LASERGENE, in der zum Anmeldezeitpunkt gültigen Fassung). Im Falle der Nukleinsäuresequenzen sind auch komplementäre oder allelische Varianten mit umfaßt. Weiterhin sind Sequenzen umfaßt, welche lediglich Teilsequenzen, beispielsweise ein Exon oder mehrere Exons, der explizit offenbarten Sequenzen oder komplementärer Sequenzen hierzu darstellen, mit der Maßgabe, daß diese Teilsequenzen im Falle der Nukleinsäuren eine für eine Hybridisierung mit einer erfindungsgemäßen Nukleinsäure hinreichende Länge, zumindest 50 oder 150 Basen, aufweisen und im Falle der Proteine bzw. Peptide, ggf. codiert durch eine Nukleinsäure, mit zumindest gleicher Affinität an ein protein- oder peptidspezifisches Zielmoleküle binden. Weiterhin sind alle mit erfindungsgemäß eingesetzten Nukleinsäuren hybridisierende Nukleinsäuren umfasst, nämlich solche, die unter stringenten Bedingungen (5°C bis 25°C unterhalb der Aufschmelztemperatur; siehe ergänzend J.M. Sambrook et al., A laboratory manual, Cold Spring Harbor Laboratory Press (1989) und E.M. Southern, J Mol Biol, 98:503ff (1975)) hybridisieren. Es versteht sich, daß die Erfindung auch Expressionskassetten umfaßt, i.e. eine oder mehrere der erfindungsgemäßen Nukleinsäuresequenzen mit mindestens einer Kontroll- oder regulatorischen Sequenz. Eine solche Expressionskassette kann auch eine Sequenz für ein bekanntes Protein umfassen, wobei im Zuge der Translation ein Fusionsprotein aus einem bekannten Protein und einem erfindungsgemäßen Protein oder Peptid entsteht. Ebenso sind auch antisense Sequenzen zu den vorstehenden Nukleinsäuresequenzen umfaßt. Mit umfaßt sind auch Expressionsvektoren enthaltend erfindungsgemäße Nukleinsäuren sowie damit transformierte Wirtszellen. Schließlich sind RNA sowie damit korrelierende DNA und umgekehrt umfaßt, ebenso wie genomische DNA als auch korrelierte cDNA und umgekehrt.

[0024] Im Zusammenhang mit erfindungsgemäßen Verwendungen umfassen die Begriffe der Nukleinsäuren oder Proteine bzw. Peptide neben den Volllängen der offenbarten Sequenzen (siehe auch vorstehender Ab-

satz) auch Teilsequenzen hieraus, und zwar mit einer Mindestlänge von 12 Nukleotiden, vorzugsweise einer Mindestlänge von 30 bis 90 Nukleotiden, im Falle der Nukleisäuren und einer Mindestlänge von 4 Aminosäuren, vorzugsweise einer Mindestlänge von 10 bis 30 Aminosäuren, im Falle der Proteine oder Peptide. Insbesondere zwischen 12 und 90 sowie 4 und 30 ist jeder einzelne Zahlenwert als Mindestlänge möglich.

[0025] Die Begriffe der Detektion und/oder der Behandlung umfassen optional auch die Detektion und/oder Behandlung von Metastasen aus Primärtumoren in sonstigen Geweben. Der Begriff der Behandlung umfasst auch die Prophylaxe sowie die Nachbehandlung (bei nicht mehr detektierbarem Tumor oder bei stabilem Tumor). Der Begriff der Prophylaxe umfasst im Zusammenhang mit der Detektion auch die Vorsorgeuntersuchung.

[0026] Als Inhibitor ist eine Verbindung oder Substanz bezeichnet, welche entweder die Bildung von des Targetmoleküls inhibiert oder gebildetes Targetmolekül in der Aktivität reduziert, bezogen auf die in vitro oder in vivo Aktivität in Abwesenheit des Inhibitors. Insofern kann ein Inhibitor einerseits eine Substanz sein, welche in der Entstehungskaskade des Targetmoleküls inhibierend eingreift. Auf der anderen Seite kann ein Inhibitor eine Substanz sein, welche mit gebildetem Targetmolekül eine Bindung eingeht, und zwar dergestalt, dass weitere physiologische Wechselwirkungen mit endogenen Substanzen zumindest reduziert sind. Als Inhibitoren können auch Moleküle dienen, die die Transkription des Targetmoleküls beeinflussen und inhibieren. Solche Moleküle können Polyamide oder Zinkfingerproteine sein, die durch Bindung an DNA-Regionen der basalen Transkriptionsmaschinerie die Transkription verhindern. Die Transkription kann indirekt auch über die Inhibierung von Transkriptionsfaktoren geschehen, die für die Transkription des Zielgens essentiell sind. Die Inhibierung solcher Transkriptionsfaktoren kann über die Bindung an sogenannte Decoy-Aptamere gewährleistet werden.

[0027] Von der Erfindung mit umfasst sind Mimikry-Moleküle. Dies sind Verbindungen, die den variablen Bereich, insbesondere den Bindungsbereich eines Antikörpers nachbilden und an gleicher Stelle eines Zielmoleküls binden wie der zu Grunde liegende Antikörper. Desweiteren fallen Anticaline und Affibodies unter den Begriff der Mimikrimoleküle.

[0028] Der Begriff der Antikörper umfaßt humane, humanisierte und nicht-humanisierte polyklonale oder monoklonale Antikörper (typischerweise in vivo hergestellt). Der Begriff umfasst desweiteren Phage-Display-Antikörper, Ribozym-Display Antikörper (Bindung des Genotyps (mRNA) und des Phänotyps (protein) an Ribosomen) und RNA-Display Antikörper (in vitro hergestellt). Der Begriff umfasst auch Antikörper, welche durch Chimerisierung, Humanisierung oder De-Immunisierung (Ausschneiden von T-Zellepitopen aus dem humanen Antikörper, die unerwünschte Immunreaktionen auslösen) modifiziert sind, sowie spezifische Fragmente der leichten und/oder der schweren Kette des variablen Bereiches zu Grunde liegender Antikörper vorstehender Art. Die Herstellung bzw. Gewinnung solcher Antikörper mit vorgegebenen Immunogenen ist dem Durchschnittsfachmann wohl vertraut und braucht nicht näher erläutert zu werden. Weiterhin umfaßt sind bispezifische Antikörper, welche einerseits an ein Auslösemolekül einer Immun-Effektorzelle (z.B. CD3, CD16, CD64) und andererseits an ein Antigen der Tumorzielzelle binden. Dies bewirkt letzendlich im Bindungsfall, daß die Tumorzelle getötet wird.

[0029] Die galenische Herrichtung einer erfindungsgemäßen pharmazeutischen Zusammensetzung kann in fachüblicher Weise erfolgen. Als Gegenionen für ionische Verbindungen kommen beispielsweise Na^+, K^+, Li^+ oder Cyclohexylammonium infrage. Geeigente feste oder flüssige galenische Zubereitungsformen sind beispielsweise Granulate, Pulver, Dragees, Tabletten, (Mikro-) Kapseln, Suppositorien, Sirupe, Säfte, Suspensionen, Emulsionen, Tropfen oder Lösungen zur Injektion (i.v., i.p., i.m., s.c.) oder Vernebelung (Aerosole), transdermale Systeme, sowie Präparate mit protrahierter Wirkstoff-Freigabe, bei deren Herstellung übliche Hilfsmittel wie Trägerstoffe, Spreng-, Binde-, Überzugs-, Quellungs-, Gleit- oder Schmiermittel, Geschmacksstoffe, Süßungsmittel und Lösungsvermittler, Verwendung finden. Als Hilfsstoffe sei Magnesiumcarbonat, Titandioxid, Lactose, Mannit und andere Zucker, Talcum, Milcheiweiß, Gelatine, Stärke, Zellulose und ihre Derivate, tierische und pflanzliche Öle wie Lebertran, Sonnenbluumen-, Erdnuss- oder Sesamöl, Polyethylenglycole und Lösungsmittel, wie etwa steriles Wasser und ein- oder mehrwertige Alkohole, beispielsweise Glycerin, genannt. Eine erfindungsgemäße pharmazeutische Zusammensetzung ist dadurch herstellbar, dass mindestens ein erfindungsgemäß verwendeter Inhibitor in definierter Dosis mit einem pharmazeutisch geeigneten und physiologisch verträglichen Träger und ggf. weiteren geeigneten Wirk-, Zusatz- oder Hilfsstoffen mit definierter Inhibitordosis gemischt und zu der gewünschten Darreichungsform hergerichtet ist.

[0030] Tumorzellen exprimieren ein Protein differenziell, wenn Normalzellen des gleichen Gewebetyps dieses nicht oder nur in sehr geringen Mengen exprimieren. Tumorzellen überexprimieren ein Protein spezifisch bzw.

differenziell, wenn dieses im Vergleich zu Normalzellen des gleichen Gewebes zumindest in doppelter Menge exprimiert wird. Es gilt Entsprechendes umgekehrt, wenn das Protein im Gegensatz zu Tumorzellen in normalen Zellen exprimiert bzw. überexprimiert wird.

[0031] Zytotoxische Komponenten bzw. Gruppen sind Verbindungen, welche direkt oder indirekt Apoptose und/oder Nekrose einleiten oder zumindest wachstumshemmend wirken. Solche Gruppen bzw. Verbindungen können neben Radioisotopen (z.B. 188Re, 213Bi, 99mTc, 90Y, 131J, 177Lu) insbesondere Toxine (z.B. Diphterie-, Pseudomonas-Toxin) oder Zytostatika einschließlich sogenannter Prodrugs sein, welche in der Tumortherapie eingesetzt werden. Beispiele hierfür sind: Alkylantien (z.B. Mechlorethamin, Ifosfamid, Chlorambucil, Cyclophosphamid, Melphalan, Alkylsulfonate, Busulphan, Nitrosoharnstoffe, Carmustin, Lomustin, Semustin, Triazene, Dacarbazin), Antimetaboliten (z.B. Folsäure-Antagonisten, Methotrexat, Pyrimidin-Analoga, Fluoruracil, Fluordesoxyuridin, Cytarabin, Gemcitabin, Purin-Analoga, Mercaptopurin), Mitosehemmer (z.B. Vincaalkaloide, Vincristin, Vinblastin, Paclitaxal, Docetaxel, Protaxel), Epipodophyllotoxine (z.B. Etoposid, Teniposid), Antibiotika (z.B. Dactinomycin, Daunorubicin, Idarubicin, Anthracycline, Bleomycin, L-Asparaginase), Platinkomplexverbindungen (z.B. Cisplatin), Hormone und verwandte Verbindungen (z.B. Nebennierensindensteroide, Aminogluthetimid, Gestagene, Östrogene, Androgene, Antiöstrogene, Tamoxifen, Steriodanaloga, Flutamid). Bei Bindung einer solchen Verbindung mit einer an das Protein bindenden Substanz erfolgt die Kopplung dergestalt, daß die Affinität zum Protein um nicht mehr als 90%, vorzugsweise 50%, bezogen auf die Substanz ohne zytostatische Gruppe, reduziert ist und die zytostatische Wirkung der Gruppe um nicht mehr als 90%, vorzugsweise 50%, bezogen auf die Verbindung ohne Substanz, reduziert ist.

[0032] Eine immunstimulierende Komponente ist meist ein Protein oder ein wirksamer Bestandteil hiervon, welches Zellen des Immunsystems stimuliert. Beispiele hierfür sind: Zytokine, wie M-CSF, GM-CSF, G-CSF, Interferone, wie IFN-alpha, beta, gamma, Interleukine wie IL-1 bis -16 (außer -8), human LIF, Chemokine wie Rantes, MCAF, MIP-1-alpha, -beta, NAP-1 und IL-8.

[0033] Eine Reportergruppe ist ein Atom, Molekül oder eine Verbindung, welche in Verbindung mit einem hierauf abgestellten Assay den Nachweis der Reportergruppe und der somit mit der Reportergruppe verbundenen Verbindung oder Substanz ermöglicht. Beispiele für Reportergruppen und hiermit assoziierte Detektionsmethoden sind: 32P-Labeling und Intensitätsmessung mittels Phosphoimager. Viele weitere Beispiele sind dem Durchschnittsfachmann bekannt und bedürfen nicht der detaillierten Aufzählung.

[0034] Eine an ein Targetmolekül bindende Substanz kann eine Substanz sein, welche ein Targetmolekül-Protein, eine Targetmolekül-RNA, oder eine Targetmolekül-DNA bindet. Mit umfasst sind dabei bezüglich der DNA auch Inhibitoren Transkription der Targetmolekül DNA und/oder Inhibitoren der die Targetmolekül-Genexpression regulierenden Region.

[0035] Im Rahmen der vorstehenden Definition gegenüber dem engen Wortsinn erweiterte Begriffsbestimmungen umfassen auch die bestimmten Begriffe im engen Wortsinn.

[0036] Vorbekannte Sequenzen und/oder deren Verwendung, welche unter die im Rahmen dieser Beschreibung verwendete Definitionen fallen, können durch einen Disclaimer in Patentansprüchen ausgeschlossen werden.

Beispiele

[0037] Im Folgenden wird die Erfindung anhand von lediglich bevorzugte Ausführungsformen darstellenden Beispielen und Figuren näher erläutert. Dabei ist Gegenstand insbesondere der Subtyp des Bronchialkarzinoms. Es zeigen:

[0038] **Fig.** 1: Chip-Analysen zur differenziellen Expression der 489 Gene in Lungentumorgewebe aus 26 Patienten (14 Patienten mit Plattenepithelkarzinom und 12 Patienten mit Adenokarzinom). Aufgetragen auf der Abzisse sind einzelne Chipexperimente von entweder Tumor- oder Normalgewebe. Die linke Ordinate stellt die relative Expression (PMQ) des Gens SeqID162/SeqID651 dar, während rechts die Signifikanz (p-Val) aufgetragen ist,

[0039] **Fig.** 2: Immunhistochemische Anfärbung der 489 Gene bzw. deren Proteine mittels spezifischer Antikörper (z.B.: SeqID162/SeqID651),

[0040] **Fig.** 3: Taqman-Analyse zur differentiellen Expression von 489 Genen im Lungentumorgewebe (nach

erfolgter Laser-gestützter Mikrodissektion der Normalepithelien und Tumorzellen) (z.B.: SeqID162/SeqID651),

[0041] **Fig.** 4: Taqman-Analyse zur spezifischen Expressionsverteilung von 489 Genen in 26 human Normalgeweben (z.B.: SeqID162/SeqID651),

[0042] **Fig.** 5: Taqman-Analyse zur differentiellen Expression von 489 Genen im Lungentumorgewebe (bulk), insbesondere im Subtyp des Plattenepithelkarzinoms, aus 11 Patienten (z.B.: SeqID162 /SeqID651),

[0043] **Fig.** 6: Northern-Blot-Verfahren des sogenannten Cancer-Profiling-Arrays zur differentiellen Expression von 489 Genen insbesondere im Brochial-, Kolon-, Mamma-, Uterus- bzw. Endometrium-, Ovarial- und Rektalkarzinomgewebe (z.B.: SeqID162/SeqID651).

[0044] **Fig.** 7: Northern-Blot-Verfahren zur sogenannten Multiple-Tissue-Analyse zur spezifischen Expression von 489 Genen in 16 Normalgeweben eines Patienten (z.B.: SeqID162/SeqID651).

[0045] **Fig.** 8: Western Blot Analyse zur Überprüfung der erhöhten Proteinexpression in Bronchialtumorgeweben von 489 Antiseren, welche spezifische ihre 489 Antigene (Proteine) detektieren (z.B.: SeqID162/SeqID651).

[0046] Entsprechende Experimente für andere Gene bzw. Sequenzen sind lediglich der Übersichtlichkeit halber nicht dargestellt.

Beispiel 1: Mikrodissektion

[0047] Bronchialtumor- und -normalgewebe aus jeweils einem Patienten wurde gefroren und in 5 µm Proben geschnitten. Aus jedem Patienten wurden zumindest 30 Proben gewonnen. Normal und maligne Bereiche wurden durch einen Pathologen mit Hilfe eines Mikroskopes identifiziert und markiert. Die jeweiligen Bereiche wurden unter dem Mikroskop resektiert unter Verwendung eines computergestützten Lasers und jeweils separat auf –80°C eingefroren in 150 µl GTC-Puffer enthaltend 2% β-Mercaptoethanol.

Beispiel 2: Chipanalyse

[0048] Aus Proben aus Beispiel 1 wird RNA isoliert, amplifiziert und markiert. Hierzu wird folgende Technik verwendet.

[0049] Die Präparation von Poly-A+-RNA erfolgt unter Verwendung eines modifizierten Protokolls gemäß dem Poly-A-Tract 1000 Kit (Promega, Deutschland). Gewebeproben werden langsam auf Eis aufgetaut, zerkleinert und mit 300 µl Verdünnungspuffer, enthaltend 1% β-Mercaptoethanol, sowie biotinyliertem Oligo-dT Primer versetzt, und für 5 min. auf 70°C erhitzt. Die Proben werden dann für 5 min. bei 20°C gehalten und anschließend bei 20000 g für 10 min. zentrifugiert. Dem Überstand werden 120 µl gewaschener Streptavidin-gekoppelter paramagnetischer Partikel (SA-PMP) zugebenen und es wurde bei 20°C für 5 min. inkubiert. Die mRNA wurde dann durch magnetische Trennung isoliert. Nach drei Waschschritten mit 0,5 × SSC Lösung wird die mRNA in Nuklease-freiem Wasser verdünnt, eingedampft unter Vakuum und umgehend wie folgt in cDNA prozessiert.

[0050] Die mRNA wird in 10 µl Nuklease-freiem Wasser gelöst. 1 µl T7-dT24-(GGCCAG) Primer (100 pmol/µl) wird zugegeben und es wird auf 70°C für 5 min. erhitzt. Dann wird die Probe auf Eis gelegt und es werden 4 µl 5× first strand buffer (Invitrogen), 2 µl DTT (0,1M), 1 µl dNTP's (10 mM), und 14U anti-RNAse (Ambion) zugegeben, gefolgt von einer Inkubation für, 2 min. bei 37°C. Dann werden 1 µl Superscript II Reverse Transskriptase (Invitrogen) zugegeben, gefolgt von einer Inkubation für 1 h bei 37°C.

[0051] Anschließend erfolgt die Zweitstrangsynthese und DNA Reinigung. Sofort nach der Synthese des ersten Stranges, wie vorstehend, werden 91 µl Wasser, 30 µl 5× second strand buffer, 3 µl dNTP's (10 mM), 10U E. coli DNA-ligase, 40U DNA Polymerase I und 2U RNAse H (alle von Invitrogen) zugegeben und die Mischung wird für 2 h bei 16°C inkubiert. Dann werden 10U T4 DNA Polymerase (Invitrogen) zugegeben und weitere 5 min, inkubiert. Die Reaktion wird durch Zugabe von 10 µl 0,5 mM EDTA abgebrochen. Die Reinigung der DNA erfolgt gemäß den Vorschriften des GFX PCR DNA and Gel Band Purification Kits (Amersham). Gereinigte DNA wird unter Vakuum eingedampft und bei –20°C gelagert.

[0052] Dann erfolgt die in vitro Transkription und cRNA Reinigung. Die in vitro Transskription wird gemäß dem

Herstellerprotokoll von Ambion (Huntigdon, UK) durchgeführt. Das DNA Pellet wird in 8 µl Wasser gelöst und 1,5 µl dNTP's (75 mM), 2 µl 10× reaction buffer (Ambion), 2 µl 10 T7 Enzymmix (Ambion) und 14U anti-RNAse (Ambion) werden zugegeben, gefolgt von einer Inkubation von 6 h bei 37°C. Die Reinigung der erhaltenen cRNA erfolgt gemäß dem Herstellerprotokoll zum Rneasy Mini Kit (Qiagen, Hilden, Deutschland). Nach Elution von der Säule wird die verdünnte cRNA eingedampft unter Vakuum und auf –80°C eingefroren.

[0053] Anschließend wird eine zweite und dritte in vitro Transskriptionsrunde durchgeführt. Diese Verstärkungsrunden werden mit nur geringen Abweichungen von der ersten Runde durchgeführt. Die Synthese des ersten Stranges erfolgt mit Random Hexamer Primern (250 ng/µl). Nach Inkubation bei 37°C für 60 min. wird das cRNA-cDNA Hybrid für 20 min. mit 2U RNase H bei 37°C inkubiert, gefolgt von einem 2-minütigen Inaktivierungsschritt bei 37°C. Die Zweitstrang-Synthese wird in dieser zweiten und dritten Runde wie oben für die erste Runde beschrieben durchgeführt. Die in vitro Transkription wird in der dritten Runde mit biotinmarkierten NTP's durchgeführt.

[0054] Die so erhaltene biotinylierte RNA wird einem Genchip aufgegeben, welcher eine Vielzahl von verschiedenen Oligonukleotiden enthält, wobei jeweils eines (oder auch mehrere, zu Kontrollzwecken) für ein definiertes Gen repräsentativ ist, i.e. eine charakteristische Teilsequenz hieraus aufweist. Man erhält sowohl qualitative, wie auch quantitative Information, ob eine betreffende Normal- und/oder Tumorprobe ein betreffendes Gen exprimiert, und zwar auch im Verhältnis Tumor/Normal. In Fällen, in welchen ein Gen in Tumorgewebe höher exprimiert ist, als im korrelierten Normalgewebe liegt diffentielle Expression vor, i.e. das Gen ist im Tumorgewebe hochreguliert. Wenn das Gen dagegen in Tumorgewebe geringer exprimiert ist, liegt Herunterregulation vor. Es wurde gefunden, dass die analysierten erfindungsgemäßen Sequenzen differenziell im Tumorgewebe reguliert sind (**Fig.** 1).

Beispiel 3: Untersuchung der Expression bzw. Überexpression mittels quantitativer PCR.

[0055] Die differenzielle Expression der Targetgene wird mittels quantitativer Echtzeit-PCR (TaqMan System) untersucht. Dazu wird die RNA, beispielsweise aber nicht notwendigerweise erhalten gemäß Beispiel 2 (cDNA nach der 1. in vitro Transkription), verwendet. 1 ng cDNA werden für die Amplifikation eingesetzt mit 2,5 µl 10× SYBR®Green PCR Puffer, 3 µl Magnesiumchlorid (25 mM), 2 µl dNTP's (mit dUTP; 12,5 mM) und 0,625U Ampli Taq Gold in einem Reaktionsvolumen von 25 µl. Die Reaktion wird in einem GeneAmp 5700 Sequence Detection System (Applied Biosystems, Weiterstadt, Deutschland) durchgeführt. Die Bedingungen sind: 2 min. 50°C, 10 min. 95°C, 15 s 95°C, 1 min. 60°C, die letzten beiden Phasen in 40 Zyklen. Für die jeweiligen Gene werden die geeigneten Vorwärts- bzw. Rückwärtsprimer verwendet. Die Auswertung erfolgt nach der ΔΔCt Methode nach Herstellervorschrift. Der Ct Wert von beta actin wurde bei einer Grenze von 0,1 gemessen. Zur Normalisierung wird der Ct Wert des beta actin vom Ct Wert des untersuchten Gens abgezogen. Dieser normalisierte Ct Wert wird im Falle der Tumorgewebe auf die Normalgewebe bezogen bzw. normalisiert, wodurch der ΔΔCt erhalten wird. Wird dieser Wert als Potenz zur Basis 2 eingesetzt, so wird eine relative Größe der Über- oder Unterexpression in Tumorgewebe gegenüber dem Normalgewebe des gleichen Patienten erhalten. Im Ergebnis kann so bestimmt werden, ob ein spezifisches Tumorgewebe eines bestimmten Patienten sensitiv für eine erfindungsgemäße Behandlung ist. Auch kann mit dieser Methode bestimmt werden, ob nicht klassifiziertes Gewebe als Tumorzellen enthaltend einzustufen ist. In letzterem Falle erfolgt ein Vergleich zu Referenzwerten bzw. klassifiziertem Normalgewebe des gleichen Patienten oder von anderen Personen.

[0056] Ergebnisse für die Überexpression des Gens Seq.-ID 162 bzw. 651 in Bronchialtumoren sind der **Fig.** 2 zu entnehmen. In der **Fig.** 4 erkennt man, dass die Expression in verschiedenen Normalgeweben sehr unterschiedlich, teilweise auch sehr hoch ist. In der Lunge wird ein nur sehr geringes Expressionsniveau festgestellt. In der **Fig.** 5 erkennt man schließlich, dass das untersuchte Gen insbesondere im Subtyp des Plattenepithelgewebes differenziell exprimiert wird. Entsprechende Ergebnisse werden mittels Northern Blots (**Fig.** 6 und 7) und Western Blots (**Fig.** 8) erhalten, wodurch auch auf Proteinebene eine Verifizierung der Ergebnisse auf Nukleinsäurenebene erfolgt.

Beispiel 4: Nachweis eines überexprimierten Gens mittels Antikörpern.

[0057] In diesem Beispiel wird die Markierung von Tumorzellen durch einen gegen ein erfindungsgemäßes Protein gerichteten Antikörper in vivo (Mausmodell) beschrieben. Ein solcher erfindungsgemäßer Antikörper wird mit einem Markermolekül (z.B. Radioisotop) markiert. In NMRI-Nacktmäuse werden mit einem erfindungsgemäßen Gen transfizierte humane Zellen transplantiert. Nach einem definierten Zeitraum, beispielsweise 30 Tage, wird den Mäusen der markierte Antikörper injiziert. Die Kontrolltiere werden mit einem nicht relevanten Antikörper behandelt. Wenige Stunden nach der Antikörperapplikation werden die Tiere getötet und aus allen

Organen Gewebeschnitte angefertigt. Diese Schnitte werden auf die Gegenwart von markiertem Antikörper untersucht.

[0058] Bei den Antikörpern kann es sich im einfachsten Fall um polyklonale Antikörper gegen humanes Protein, konjugiert mit einem Trägerprotein, in Kaninchen gezogen und mit den spezifischen immobilisierten Peptiden affinitätsgereinigt, handeln. Geeignete Immunisierungspeptide sind beispielsweise aus Teilsequenzen eines erfindungsgemäßen Proteins gebildet. Als Immunogene können ebenso mit cDNA des Gens, oder Teilsequenzen hiervon transfizierte Zellen, wie beispielsweise COS-Zellen oder NIH3T3-Zellen, eingesetzt werden. Ebenso sind Tumorzellen, die endogen das Protein exprimieren, geeignet. Weiterhin kann auch rekombinant hergestelltes Protein bzw. Teilsequenzen hieraus, die in Producerzellen, wie E. coli oder Eukaryontenzellen, wie Insektenzellen, exprimiert werden, zur Immunisierung eingesetzt werden. Selbstverständlich können stattdessen auch entsprechende monoklonale Antikörper oder Fragmente hiervon eingesetzt werden.

[0059] Das hier untersuchte Gen zeigt gemäß der **Fig.** 2 eine vergleichsweise starke Färbung in Plattenepithelkarzinomgewebe.

Beispiel 5: Immunhistochemischer Nachweis von Tumorzellen.

[0060] Gewebe wird aus einem Patienten mit Krebs oder dem Verdacht auf Krebs isoliert und als Paraffin- bzw. Gefrierschnitte präpariert. Diese Schnitte werden mit einem gegen ein erfindungsgemäßes Protein gerichteten Antikörper auf die Überexpression des Proteins in Tumorzellen untersucht. Die immunhistologische Untersuchung mit dem Antikörper zeigt höhere Expression des Proteins in den Tumorzellen im Vergleich zu umliegenden Normalgewebe. Die Untersuchung erfolgt im Einzelnen durch Inkubation mit dem Antikörper als primärem Antikörper, einem biotinyliertem sekundären anti-Kaninchen Antikörper und einer Streptavidin-gekoppelten Meerrettichperoxidase. Die Färbung erfolgt mit mit DAB als chromogenen Substrat (braune Färbung). Die Gegenfärbung erfolgt mit Hemalaun-Lösung (blaue Färbung). Es sind maligne und nichtmaligne Zellen unterscheidbar, wobei die malignen Zellen eine starke Färbung, i.e. hohen Gehalt an erfindungsgemäßem Protein, aufweisen, während die nichtmalignen Zellen nur moderat gefärbt sind.

[0061] Im Falle einer Erkrankung erkennt man im Falle der Überexpression in Tumorgewebe eine vergleichsweise starke Färbung.

Beispiel 6: Erzeugung von anti-idiotypischen monoklonalen Antikörpern zu therapeutischen Zwecken

[0062] Ausgehend von einem erfindungsgemäßen Protein wird in fachüblicher Weise ein monoklonaler Antikörper Ab1 erzeugt, welcher in der Lage ist, das beispielsweise das Protein Seq.-ID 651 spezifisch zu erkennen und daran zu binden. Dabei ist es unwesentlich, ob eine funktionale Domäne oder ein anderer zugänglicher Bereich erkannt wird. Mit Hilfe des erzeugten Antikörpers Ab1 wird in ebenso fachüblicher Weise ein zweiter anti-idiotypischer nicht humanisierter, beispielsweise Maus, monoklonaler Antikörper aAB1 erzeugt, welcher zur Herstellung einer pharmazeutischen Zusammensetzung zur Behandlung von Bronchialtumoren geeignet ist. Die Funktion des Antikörpers aAB1 beruht dabei darauf, dass dieser dem humanen Immunsystem ein Image des (humanen) Protein-Antigens gleichsam vortäuscht, wobei das Immunsystem den Antikörper aAB1 aufgrund seiner mangelnden Humanisierung als körperfremd erkennt. Der humane Körper bildet folglich eigene Antikörper, die gegen aAB1 und somit auch gegen das humane Protein bzw. dieses exprimierende Tumorzellen gerichtet sind.

UGCluster	Hs.101915
2=nur AD 1=auch SCC	0
Seq_NR	1
Pep_NR	490
Probeset	219532_at
227958	219532_at
CF2_rule1(Paired)	8
CF3_rule1	5
CF4_rule1	3
CF8_rule1	0
CFs05_rule1	0
Missing_rule1	5
Rank_Golub	668
Rank_CFM	532
CHIPLISTID	2
TRANSMEMBRANE_AUTO	1
KINASE_AUTO	
PROTEASE_AUTO	
SECRETED_AUTO	
DRUGABLE_AUTO	1
PHOSPHATASE_AUTO	
OTHER_ENZYMES_AUTO	
ANNOTATION	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219532_at&chip_id=2
WEBLINK	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=101915
WEBLINK	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=101915
Header	Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (ELOVL4), mRNA /cds=(147,1091) /gb=NM_022726 /gi=12232378 /ug=Hs.101915 /len=2900
UGCluster	Hs.101915
hat	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
gpr87	ELOVL4

Hs.103291	0	2	491	**218625_at**	**218625_at**	8	8	6	1	0	1	554	223	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218625_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103291	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103291	Homo sapiens neuritin (LOC51299), mRNA /cds=(168,596) /gb=NM_016588 /gi=7706122 /ug=Hs.103291 /len=1589	Hs.103291	neuritin	LOC51299
Hs.104222	0	3	492	**222442_s_at**	**222442_s_at**	12	11	7	0	0	0	276.	296	3		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222442_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104222	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104222	Homo sapiens hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(174,734) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	Hs.104222	hypothetical protein FLJ10702	FLJ10702

Hs.106552	0	4	493	219301_s_at	219301_s_at	9	7	7	3	1	2	700	211	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219301_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106552	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106552	Homo sapiens contactin-associated protein 2 (CNTNAP2) mRNA, complete cds /cds=(140,4135) /gb=AF319045 /gi=13624213 /ug=Hs.106552 /len=8107	Hs.106552	contactin associated protein-like 2	CNTNAP2
Hs.108338	0	5	494	223334_at	223334_at	6	1	0	0	0	0	319	1086	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223334_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108338	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108338	Homo sapiens hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(105,692) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	Hs.108338	hypothetical protein DKFZp586C1924	DKFZp586C1924

Hs.108923	0	6	495	**219412_at**	**219412_at**	8	6	5	2	1	1	660	603	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219412_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108923	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108923	Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA /cds=(47,682) /gb=NM_022337 /gi=11641236 /ug=Hs.108923 /len=1412	Hs.108923	RAB38, member RAS oncogene family	RAB38

Hs.112341	0	7	496	**203691_at**	**203691_at**	5	5	5	4	2	7	914	234	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203691_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112341	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112341	Homo sapiens protease inhibitor 3, skin-derived (SKALP) (PI3), mRNA /cds=(119,472) /gb=NM_002638 /gi=4505786 /ug=Hs.112341 /len=631	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	PI3

Hs.114670
LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE
[H.sapiens]

Hs.114670
0
8
497
231897_at
231897_at
231897_at
7 5 4 2 3 0
912
1202
3

1 1 &chip_id=3 4670 4670 70 /len=1219
d=231897_at =Hs&CID=11 =Hs&CID=11 /ug=Hs.1146
pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=18516040
obeset_anno. v/UniGene/cl v/UniGene/cl 98
eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=BM4669
bin/eike/prob http://www.nc http://www.nc '
gi-
metagen.de/c
http://intranet.
/clone_end=5
E:5572905
/clone=IMAG
cDNA, 5' end
sapiens
Homo
T_6471991
AGENCOUR

Hs.115242	0	9	498	**202810_at**	**202810_at**	7	0	0	0	0	0	384	1333	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202810_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115242	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115242	Homo sapiens developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(65,1168) /gb=NM_004147 /gi=4758795 /ug=Hs.115242 /len=1383	Hs.115242	developmentally regulated GTP binding protein 1	DRG1

Hs.11806	0	10	499	**201791_s_at**	**201791_s_at**	12	7	5	1	1	0	595	380	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201791_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11806	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11806	Homo sapiens 7-dehydrocholesterol reductase (DHCR7), mRNA /cds=(194,1621) /gb=NM_001360 /gi=4503320 /ug=Hs.11806 /len=2597	Hs.11806	7-dehydrocholesterol reductase DHCR7

Hs.119693	0	11	500	**223629_at**	**223629_at**	7	6	6	0	2	5	907	583	3	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223629_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=119693	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=119693	Homo sapiens protocadherin beta 5 (PCDHB5), mRNA /cds=(217,2604) /gb=NM_015669 /gi=14195611 /ug=Hs.119693 /len=2925	Hs.119693	protocadherin beta 5 PCDHB5

Hs.120165	0	12	501	**218939_at**	**218939_at**	1	0	0	0	0	13	336	1505	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218939_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=120165	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=120165	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1 (LETM1), mRNA /cds=(297,2516) /gb=NM_012318 /gi=6912481 /ug=Hs.120165 /len=3907	Hs.120165	leucine zipper-EF-hand containing transmembrane protein 1	LETM1

Hs.12152	0	13	502	**227737_at**	**227737_at**	4	2	0	0	0	0	302	1436	3	1	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=227737_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=12152	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=12152	Homo sapiens APMCF1 protein (APMCF1), mRNA /cds=(16,831) /gb=NM_021203 /gi=14917112 /ug=Hs.12152 /len=1745	Hs.12152	APMCF1 protein	APMCF1

Hs.125180	0	14	503	**205498_at**	**205498_at**	6	4	4	1	1	2	856	1017	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205498_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=125180	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=125180	Homo sapiens growth hormone receptor (GHR), mRNA /cds=(43,1959) /gb=NM_000163 /gi=4503992 /ug=Hs.125180 /len=4414	Hs.125180	growth hormone receptor	GHR

Hs.127287	0	15	504	212840_at	212840_at	11	7	5	0	0	0	461	428	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212840_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=127287	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=127287	Homo sapiens mRNA for KIAA0794 protein, partial cds /cds=UNKNOWN /gb=AB018337 /gi=3882308 /ug=Hs.127287 /len=4656	Hs.127287	KIAA0794 protein KIAA0794
Hs.13034	0	16	505	235022_at	235022_at	11	8	8	0	1	0	324	183	3	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=235022_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13034	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13034	Homo sapiens cDNA FLJ31056 fis, clone HSYRA2000760 /cds=(388,1206) /gb=AK055618 /gi=16550393 /ug=Hs.13034 /len=1941	Hs.13034	Homo sapiens cDNA FLJ31056 fis, clone HSYRA2000760

Hs.13094	0	17	506	**218271_s_at**	**218271_s_at**	9	1	0	0	0	0	305	1228	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218271_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13094	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13094	Homo sapiens presenilins associated rhomboid-like protein (PARL), mRNA /cds=(0,1139) /gb=NM_018622 /gi=14249121 /ug=Hs.13094 /len=1140	Hs.13094	presenilins associated rhomboid-like protein	PARL
Hs.1342	0	18	507	**211025_x_at**	**211025_x_at**	10	2	1	0	0	0	402	860	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211025_x_at&chip_id=242	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1342	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1342	Homo sapiens cytochrome c oxidase subunit Vb (COX5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(29,418) /gb=NM_001862 /gi=17017987 /ug=Hs.1342 /len=523	Hs.1342	cytochrome c oxidase subunit Vb	COX5B

Hs.137569	0	19	508	209863_s_at	209863_s_at	12	10	9	2	0	0	445	190	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209863_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=137569	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=137569	Homo sapiens mRNA for KET protein /cds=(27,2069) /gb=Y16961 /gi=3970716 /ug=Hs.137569 /len=4849	Hs.137569	tumor protein p63	TP63
Hs.13794	0	20	509	222417_s_at	222417_s_at	9	8	5	0	1	1	472	387	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222417_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13794	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13794	Homo sapiens sorting nexin 5 (SNX5), mRNA /cds=(86,1300) /gb=NM_014426 /gi=7657598 /ug=Hs.13794 /len=2056	Hs.13794	sorting nexin 5	SNX5

Hs.1390	0	21	510	**200039_s_at**	**200039_s_at**	8	2	0	0	0	0	382	882	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200039_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1390	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1390	Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, clone MGC:1664 IMAGE:3352313, mRNA, complete cds /cds=(58,663) /gb=BC000268 /gi=12653014 /ug=Hs.1390 /len=2044	Hs.1390	proteasome (prosome, macropain) subunit, beta type, 2	PSMB2

Hs.139851	0	22	511	203324_s_at	203324_s_at	10	4	3	0	1	0	889	433	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203324_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=139851	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=139851	Homo sapiens caveolin 2 (CAV2), mRNA /cds=(181,669) /gb=NM_001233 /gi=15451857 /ug=Hs.139851 /len=1483	Hs.139851	caveolin 2	CAV2

transcription termination factor, RNA polymerase II
TTF2

Hs.142157

Homo
sapiens
lodestar
protein
mRNA,
complete cds
/cds=(30,351
gi-
bin/eike/prob http://www.nc http://www.nc 8)
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1

2
432
641
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1
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4
5
9

204407_at
204407_at
512
23
0

Hs.142157

Hs.143600	0	24	513	**204324_s_at**	**204324_s_at**	8	6	3	0	0	1	526	401	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204324_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=143600	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=143600	Homo sapiens type II Golgi membrane protein (GPP130), mRNA /cds=(13,2103) /gb=NM_014498 /gi=7657137 /ug=Hs.143600 /len=2506	Hs.143600	golgi phosphoprotein 4	GOLPH4

Hs.152213	0	25	514	**205990_s_at**	**205990_s_at**	8	6	4	2	0	0	746	796	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205990_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152213	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152213	Homo sapiens wingless-type MMTV integration site family, member 5A (WNT5A), mRNA /cds=(757,1854) /gb=NM_003392 /gi=17402917 /ug=Hs.152213 /len=4428	Hs.152213	wingless-type MMTV integration site family, member 5A WNT5A

Hs.15243	0	26	515	**214427_at**	**214427_at**	4	1	0	0	0	6	152	1032	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=214427_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=15243	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=15243	Homo sapiens nucleolar protein 1 (120kD) (NOL1), mRNA /cds=(0,2567) /gb=NM_006170 /gi=5453791 /ug=Hs.15243 /len=2568	Hs.15243	nucleolar protein 1 (120kD) NOL1

Hs.153591

0

27

516

207396_s_at

207396_s_at

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1 1

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bin/eike/prob http://www.nc http://www.nc 7)

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http://intranet.

mRNA

/cds=(31,134

(NOT56L),

)-like protein

melanogaster

Not56 (D.

sapiens

Homo

Hs.153591

Not56 (D. melanogaster)-like protein

NOT56L

Hs.154294	0	28	517	**202514_at**	**202514_at**	11	9	7	1	1	0	478	398	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202514_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154294	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154294	Homo sapiens discs, large (Drosophila) homolog 1 (DLG1), mRNA /cds=(188,2968) /gb=NM_004087 /gi=4758161 /ug=Hs.154294 /len=3046	Hs.154294	discs, large (Drosophila) homolog 1	DLG1

Hs.154443	0	29	518	**212141_at**	**212141_at**	1	0	0	0	0	13	162	519	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212141_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154443	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154443	H.sapiens P1-Cdc21 mRNA /cds=(0,2773) /gb=X74794 /gi=683749 /ug=Hs.154443 /len=3273	Hs.154443	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	MCM4

Hs.154510	0	30	519	**205379_at**	**205379_at**	7	6	5	2	1	5	842	703	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205379_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154510	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=154510	Homo sapiens carbonyl reductase 3 (CBR3), mRNA /cds=(22,855) /gb=NM_001236 /gi=7108334 /ug=Hs.154510 /len=900	Hs.154510	carbonyl reductase 3 CBR3

Hs.155324	0	31	520	**203878_s_at**	**203878_s_at**	3	1	0	0	0	11	303	1330	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203878_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155324	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155324	Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA /cds=(22,1488) /gb=NM_005940 /gi=13027795 /ug=Hs.155324 /len=2260	Hs.155324	matrix metalloproteinase 11 (stromelysin 3) MMP11

Hs.155787	0	32	521	**211702_s_at**	**211702_s_at**	6	1	0	0	0	0	183	1065	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211702_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155787	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155787	Homo sapiens ubiquitin specific protease (NY-REN-60), mRNA /cds=(0,3824) /gb=NM_032582 /gi=14211902 /ug=Hs.155787 /len=3825	Hs.155787	ubiquitin specific protease	NY-REN-60

Hs.158159	0	33	522	**208153_s_at**	**208153_s_at**	9	5	3	1	1	3	1152	429	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208153_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=158159	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=158159	Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA /cds=(13,13062) /gb=NM_001447 /gi=13787216 /ug=Hs.158159 /len=14536	Hs.158159	FAT tumor suppressor homolog 2 (Drosophila) FAT2

Hs.161786
0
34
523
221698_s_at
221698_s_at
5 5 4 2 3 1
986
1914
2 1
1 1
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Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12), mRNA /cds=(71,676)
Hs.161786
C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12
CLECSF12

Hs.1640	0	35	524	**204136_at**	**204136_at**	11	7	5	2	1	0	925	258	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204136_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1640	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1640	Homo sapiens collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive) (COL7A1), mRNA /cds=(98,8932) /gb=NM_000094 /gi=17738300 /ug=Hs.1640 /len=9272	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)	COL7A1

Hs.164280

0

36

525

212085_at

212085_at

212085_at

7 5 4 1 0 0 0 1

851

802

2 1

1

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http://intranet.

/cds=(88,984

complete cds

722, mRNA,

IMAGE:3342

MGC:3042

clone

member 5,

translocator),

nucleotide

adenine

I carrier;

(mitochondria

family 25

solute carrier

Similar to

sapiens,

Homo

solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6

SLC25A6

Hs.164280

Hs.165843	0	37	526	**211623_s_at**	**211623_s_at**	12	9	3	0	0	0	136	456	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211623_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=165843	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=165843	Homo sapiens casein kinase 2, beta polypeptide (CSNK2B), mRNA /cds=(340,987) /gb=NM_001320 /gi=10334850 /ug=Hs.165843 /len=1128	Hs.165843	casein kinase 2, beta polypeptide	CSNK2B

Hs.1690	0	38	527	**205014_at**	**205014_at**	7	7	6	3	1	1	875	259	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205014_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1690	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1690	Homo sapiens heparin-binding growth factor binding protein (HBP17), mRNA /cds=(97,801) /gb=NM_005130 /gi=4826753 /ug=Hs.1690 /len=1163	Hs.1690	heparin-binding growth factor binding protein HBP17

Hs.169610	0	39	528	**204490_s_at**	**204490_s_at**	12	11	7	2	1	0	831	336	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204490_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169610	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169610	Homo sapiens mRNA for transmembrane glycoprotein (CD44 gene) /cds=(178,2406) /gb=AJ251595 /gi=6491738 /ug=Hs.169610 /len=3091	Hs.169610	CD44 antigen (homing function and Indian blood group system) CD44

Hs.169902	0	40	529	**201250_s_at**	**201250_s_at**	13	10	6	1	0	0	88	242	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201250_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169902	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169902	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA /cds=(179,1657) /gb=NM_006516 /gi=5730050 /ug=Hs.169902 /len=2856	Hs.169902	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1

Hs.171280	0	41	530	**202282_at**	**202282_at**	10	4	3	0	0	0	425	746	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202282_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=171280	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=171280	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase, type II (HADH2), mRNA /cds=(27,812) /gb=NM_004493 /gi=4758503 /ug=Hs.171280 /len=990	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, type II	HADH2

Hs.173859	0	42	531	**203706_s_at**	**203706_s_at**	12	8	7	2	0	2	637	206	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203706_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=173859	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=173859	Homo sapiens frizzled homolog 7 (Drosophila) (FZD7), mRNA /cds=(61,1785) /gb=NM_003507 /gi=4503832 /ug=Hs.173859 /len=3851	Hs.173859	frizzled homolog 7 (Drosophila)	FZD7

Hs.17481	0	43	532	**212165_at**	**212165_at**	10	3	1	0	0	0	204	788	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212165_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=17481	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=17481	Homo sapiens my048 protein (my048), mRNA /cds=(606,1289) /gb=NM_080390 /gi=17933773 /ug=Hs.17481 /len=1487	Hs.17481	hypothetical protein BC013073	LOC92703
Hs.179902	0	44	533	**224596_at**	**224596_at**	10	8	4	1	1	0	690	577	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224596_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=179902	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=179902	Homo sapiens CDw92 antigen (CDW92), mRNA /cds=(42,2015) /gb=NM_080546 /gi=18034691 /ug=Hs.179902 /len=4301	Hs.179902	CDw92 antigen	CDW92

Hs.18136	0	45	534	**202783_at**	**202783_at**	9	4	4	0	0	1	305	531	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202783_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=18136	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=18136	Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA /cds=(43,3303) /gb=NM_012343 /gi=6912535 /ug=Hs.18136 /len=3567	Hs.18136	nicotinamide nucleotide transhydrogenase	NNT

Hs.182429	0	46	535	**207668_x_at**	**207668_x_at**	8	6	5	3	1	0	619	894	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=207668_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182429	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182429	Homo sapiens, clone MGC:20253 IMAGE:4647654, mRNA, complete cds /cds=(20,1165) /gb=BC012142 /gi=15082450 /ug=Hs.182429 /len=3033	Hs.182429	protein disulfide isomerase-related protein P5

Hs.183655	0	47	536	**218703_at**	**218703_at**	3	0	0	0	0	0	396	1262	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218703_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=183655	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=183655	Homo sapiens sec22 homolog (SEC22A), mRNA /cds=(61,984) /gb=NM_012430 /gi=14591918 /ug=Hs.183655 /len=1776	Hs.183655	sec22 homolog	SEC22A

Hs.184161	0	48	537	**201995_at**	**201995_at**	12	4	2	0	0	0	275	537	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201995_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184161	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184161	Homo sapiens exostoses (multiple) 1 (EXT1), mRNA /cds=(772,3012) /gb=NM_000127 /gi=4557570 /ug=Hs.184161 /len=3304	Hs.184161	exostoses (multiple) 1 EXT1

Hs.184456	0	49	538	**223335_at**	**223335_at**	8	1	0	0	0	0	55	917	3	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223335_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184456	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184456	Homo sapiens hypothetical protein (LOC51249), mRNA /cds=(0,611) /gb=NM_016486 /gi=7706026 /ug=Hs.184456 /len=612	Hs.184456	hypothetical protein LOC51249	LOC51249
Hs.184627	0	50	539	**203885_at**	**203885_at**	9	6	5	0	1	0	700	627	2		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203885_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184627	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184627	Homo sapiens KIAA0118 protein (KIAA0118), mRNA /cds=(255,932) /gb=NM_014999 /gi=7661921 /ug=Hs.184627 /len=2630	Hs.184627	RAB21, member RAS oncogene family	RAB21

Hs.187958	0	51	540	**210854_x_at**	**210854_x_at**	7	2	0	0	0	4	94	720	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210854_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=187958	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=187958	Homo sapiens solute carrier family 6 (neurotransmitter transporter, creatine), member 8 (SLC6A8), mRNA /cds=(638,2545) /gb=NM_005629 /gi=5032096 /ug=Hs.187958 /len=3917	Hs.187958	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	SLC6A8

Hs.193974	0	52	541	**205770_at**	**205770_at**	6	4	4	1	0	8	692	633	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205770_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=193974	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=193974	Homo sapiens glutathione reductase (GSR), mRNA /cds=(104,1543) /gb=NM_000637 /gi=10835188 /ug=Hs.193974 /len=1618	Hs.193974	glutathione reductase	GSR

Hs.194148	0	53	542	**202932_at**	**202932_at**	8	7	5	0	1	0	583	768	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202932_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194148	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194148	Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA /cds=(207,1838) /gb=NM_005433 /gi=4885660 /ug=Hs.194148 /len=4517	Hs.194148

v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
YES1

Hs.196384	0	54	543	**204748_at**	**204748_at**	5	4	4	1	4	1	1284	2211	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204748_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=196384	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=196384	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA /cds=(134,1948) /gb=NM_000963 /gi=4506264 /ug=Hs.196384 /len=4465	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	PTGS2

Hs.198427	0	55	544	**202934_at**	**202934_at**	11	9	7	3	0	2	354	80	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202934_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=198427	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=198427	H.sapiens HK2 mRNA for hexokinase II /cds=(1490,4243) /gb=Z46376 /gi=587201 /ug=Hs.198427 /len=5292	Hs.198427	hexokinase 2	HK2

Hs.2030	0	56	545	**203887_s_at**	**203887_s_at**	5	4	4	1	1	5	889	1627	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203887_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2030	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2030	Homo sapiens thrombomodulin (THBD), mRNA /cds=(541,2268) /gb=NM_000361 /gi=4507482 /ug=Hs.2030 /len=4050	Hs.2030	thrombomodulin THBD

Hs.203963	0	57	546	**223556_at**	**223556_at**	9	6	2	0	0	2	258	507	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223556_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=203963	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=203963	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds /cds=(105,2621) /gb=AF155827 /gi=8980659 /ug=Hs.203963 /len=3165	Hs.203963	helicase, lymphoid-specific	HELLS

Hs.2057	0	58	547	**202706_s_at**	**202706_s_at**	5	2	0	0	0	1	417	1219	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202706_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2057	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2057	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), mRNA /cds=(104,1546) /gb=NM_000373 /gi=4507834 /ug=Hs.2057 /len=2244	Hs.2057	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	UMPS

Hs.211579	0	59	548	**211042_x_at**	**211042_x_at**	9	6	5	1	0	0	450	502	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211042_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211579	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211579	Homo sapiens melanoma adhesion molecule (MCAM), mRNA /cds=(26,1966) /gb=NM_006500 /gi=5729917 /ug=Hs.211579 /len=3583	Hs.211579	melanoma cell adhesion molecule	MCAM

Hs.22209	0	60	549	223235_s_at	223235_s_at	5	5	4	3	2	4	970	1908	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223235_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22209	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22209	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1989266 /cds=UNKNOWN /gb=AJ420521 /gi=17066385 /ug=Hs.22209 /len=3106	Hs.22209	secreted modular calcium-binding protein 2	SMOC2

Hs.2248
0
61
550
204533_at
204533_at
204533_at
6 4 4 3 0 6 747 1377 2 1 1 1
http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info?probeset_id=204533_at&chip_id=2 48 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22 48 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22 48
Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 10 (SCYB10), mRNA /cds=(66,362) /gb=NM_001565 /gi=4504700 /ug=Hs.2248 /len=1172
Hs.2248
small inducible cytokine subfamily B (Cys-X-Cys), member 10
SCYB10

Hs.2258	0	62	551	**205680_at**	**205680_at**	7	6	5	3	4	1	1071	360	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205680_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2258	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2258	Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), mRNA /cds=(22,1452) /gb=NM_002425 /gi=4505204 /ug=Hs.2258 /len=1743	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	MMP10

Hs.227730	0	63	552	**201656_at**	**201656_at**	13	10	8	1	1	0	532	203	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201656_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=227730	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=227730	Homo sapiens integrin, alpha 6 (ITGA6), mRNA /cds=(146,3367) /gb=NM_000210 /gi=4557674 /ug=Hs.227730 /len=5611	Hs.227730	integrin, alpha 6 ITGA6

Hs.227750	0	64	553	**218226_s_at**	**218226_s_at**	9	3	1	0	0	0	235	1028	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218226_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=227750	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=227750	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) (NDUFB4), mRNA /cds=(8,397) /gb=NM_004547 /gi=6041668 /ug=Hs.227750 /len=464	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15)	NDUFB4

Hs.23016	0	65	554	**212977_at**	**212977_at**	10	9	6	0	1	0	773	432	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212977_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23016	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23016	Human orphan G protein-coupled receptor (RDC1) mRNA, partial cds /cds=(0,908) /gb=U67784 /gi=1617516 /ug=Hs.23016 /len=1716	Hs.23016	G protein-coupled receptor	RDC1
Hs.23643	0	66	555	**218499_at**	**218499_at**	10	7	3	1	0	0	354	535	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218499_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23643	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23643	Homo sapiens serine/threonine protein kinase MASK (MST4), mRNA /cds=(220,1470) /gb=NM_016542 /gi=15011879 /ug=Hs.23643 /len=3263	Hs.23643	Mst3 and SOK1-related kinase	MST4

Hs.236720	0	67	556	**223587_s_at**	**223587_s_at**	0	0	0	0	0	14	357	1564	3	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223587_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=236720	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=236720	Homo sapiens amnionless protein (AMN), mRNA /cds=(22,1383) /gb=NM_030943 /gi=13569914 /ug=Hs.236720 /len=1896	Hs.236720	amnionless protein	AMN
Hs.241407	0	68	557	**217272_s_at**	**217272_s_at**	8	6	6	2	0	2	948	427	2	1	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217272_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241407	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241407	Homo sapiens mRNA for hurpin, clone R7-1.1 /cds=(102,1277) /gb=AJ001696 /gi=6018505 /ug=Hs.241407 /len=3143	Hs.241407	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13	SERPINB13

Hs.241543	0	69	558	**222425_s_at**	**222425_s_at**	1	0	0	0	0	10	193	1577	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222425_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241543	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241543	Homo sapiens DKFZP586F1524 protein (DKFZP586F1524), mRNA /cds=(49,1155) /gb=NM_015584 /gi=7661671 /ug=Hs.241543 /len=2100	Hs.241543	DKFZP586F1524 protein	DKFZP586F1524

Hs.241551	0	70	559	**206165_s_at**	**206165_s_at**	8	8	7	2	2	0	1067	182	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206165_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241551	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241551	Homo sapiens chloride channel, calcium activated, family member 2 (CLCA2), mRNA /cds=(108,2939) /gb=NM_006536 /gi=12025665 /ug=Hs.241551 /len=3671	Hs.241551	chloride channel, calcium activated, family member 2	CLCA2

Hs.241576

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222543_at

222543_at

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1235

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http://www.nc
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v/UniGene/cl
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=Hs&CID=24
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http://www.nc
bi.nlm.nih.go
v/UniGene/cl
ust.cgi?ORG
=Hs&CID=24
1576

Homo
sapiens
hypothetical
protein
PRO2577
(PRO2577),
mRNA
/cds=(491,66
4)
/gb=NM_018
630
/gi=8924181
/ug=Hs.2415
76 /len=1032

Hs.241576

hypothetical protein PRO2577
PRO2577

Hs.24395	0	72	561	**222484_s_at**	**222484_s_at**	11	11	10	8	1	1	273	15	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222484_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24395	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24395	Homo sapiens NJAC protein (NJAC) mRNA, complete cds /cds=(7,306) /gb=AF144103 /gi=5059165 /ug=Hs.24395 /len=1503	Hs.24395	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK) SCYB14

Hs.249184	0	73	562	**223274_at**	**223274_at**	2	1	0	0	0	12	328	1268	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223274_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=249184	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=249184	SC1=putative trans-acting factor involved in cell cycle control [human, mRNA, 2481 nt] /cds=(375,1451) /gb=S53374 /gi=809488 /ug=Hs.249184 /len=2481	Hs.249184	transcription factor 19 (SC1) TCF19

Hs.26890	0	74	563	218592_s_at	218592_s_at	9	4	4	0	0	0	385	582	2	1.	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218592_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=26890	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=26890	Homo sapiens cat eye syndrome chromosome region, candidate 5 (CECR5), mRNA /cds=(26,1297) /gb=NM_017829 /gi=15277336 /ug=Hs.26890 /len=1815	Hs.26890	cat eye syndrome chromosome region, candidate 5	CECR5
Hs.271277	0	75	564	223468_s_at	223468_s_at	8	4	3	2	0	1	757	435	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223468_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271277	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271277	Homo sapiens mRNA; cDNA DKFZp434D0727 (from clone DKFZp434D0727); complete cds /cds=(96,1448) /gb=AL136826 /gi=12053162 /ug=Hs.271277 /len=3066	Hs.271277	hypothetical protein from EUROIMAGE 363668	LOC56963

Hs.271580	0	76	565	**210064_s_at**	**210064_s_at**	5	4	4	3	2	6	978	1166	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210064_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271580	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271580	Homo sapiens, Similar to uroplakin 1B, clone MGC:8896 IMAGE:3858834, mRNA, complete cds /cds=(55,588) /gb=BC012851 /gi=15277496 /ug=Hs.271580 /len=2032	Hs.271580	uroplakin 1B	UPK1B

Hs.271980	0	77	566	**207121_s_at**	**207121_s_at**	8	5	3	0	0	0	230	710	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=207121_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271980	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271980	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA /cds=(756,2921) /gb=NM_002748 /gi=16306569 /ug=Hs.271980 /len=4193	Hs.271980	mitogen-activated protein kinase 6	MAPK6

Hs.273234

0

78

567

225309_at

225309_at

12 8 3 0 0 0 0 10 33 3

1

1 &chip_id=3 3234 3234 34 /len=1097

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eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_032

bin/eike/prob http://www.nc http://www.nc)

gi-

/cds=(43,375

mRNA

(MGC1346),

MGC1346

protein

hypothetical

sapiens

Homo

http://intranet.

metagen.de/c

hypothetical protein MGC1346

MGC1346

Hs.273234

Hs.274404	0	79	568	**201860_s_at**	**201860_s_at**	11	7	5	1	2	1	667	433	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201860_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274404	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274404	Homo sapiens plasminogen activator, tissue (PLAT), transcript variant 1, mRNA /cds=(208,1896) /gb=NM_000930 /gi=14702165 /ug=Hs.274404 /len=2653	Hs.274404	plasminogen activator, tissue PLAT

Hs.274543	0	80	569	**225158_at**	**225158_at**	11	8	5	0	0	0	232	477	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225158_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274543	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274543	Homo sapiens mitochondrial elongation factor G (EFG1), mRNA /cds=(107,2362) /gb=NM_024996 /gi=18390330 /ug=Hs.274543 /len=3463	Hs.274543	mitochondrial elongation factor G	EFG1
Hs.274691	0	81	570	**204347_at**	**204347_at**	9	4	4	1	0	5	99	493	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204347_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274691	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274691	Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, mRNA /cds=(183,854) /gb=NM_013410 /gi=8051578 /ug=Hs.274691 /len=1707	Hs.274691	adenylate kinase 3	AK3

Hs.275732	0	82	571	**215812_s_at**	**215812_s_at**	7	6	1	0	0	7	73	321	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215812_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=275732	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=275732	Human creatine transporter (SLC6A10) gene, partial cds /cds=(0,1280) /gb=U41163 /gi=1209100 /ug=Hs.275732 /len=1281	Hs.275732	ESTs, Highly similar to G02277 creatine transporter [H.sapiens]	uk6

Hs.27693	0	83	572	**222500_at**	**222500_at**	1	0	0	0	0	9	410	1499	3			1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222500_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=27693	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=27693	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA /cds=(227,727) /gb=NM_016059 /gi=7706338 /ug=Hs.27693 /len=1024	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	PPIL1
Hs.278605	0	84	573	**223054_at**	**223054_at**	10	6	2	1	0	0	336	452	3	1	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223054_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=278605	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=278605	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 11 (DNAJB11), mRNA /cds=(20,1096) /gb=NM_016306 /gi=7706494 /ug=Hs.278605 /len=1159	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, member 11	DNAJB11

UDP glycosyltransferase 1 family, polypeptide A1
UGT1A1

Hs.278896

Homo sapiens UDP glycosyltransferase 1 family, polypeptide A1 (UGT1A1), mRNA /cds=(15,1616)

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215125_s_at&chip_id=2

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/gb=NM_000463 /gi=8850235 /ug=Hs.278896 /len=2351

8896 8896

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0

Hs.278896

10 10 8 2 0 1 693 177 2 1

Hs.284239	0	86	575	**206094_x_at**	**206094_x_at**	10	6	4	1	0	2	696	517	2	1	1	1	http://intranet. metagen.de/c gi- bin/eike/prob eset_anno/pr obeset_anno. pl?probeset_i d=206094_x_ at&chip_id=2	http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=28 4239	http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=28 4239	Homo sapiens UDP glycosyltransf erase 1 family, polypeptide A6 (UGT1A6), mRNA /cds=(87,168 2) /gb=NM_001 072 /gi=4507814 /ug=Hs.2842 39 /len=2422	Hs.284239	UDP glycosyltransferase 1 family, polypeptide A6 UGT1A6

Hs.284275	0	87	576	**208875_s_at**	**208875_s_at**	12	10	9	3	1	0	529	153	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208875_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284275	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284275	Homo sapiens PAK2 mRNA, complete cds /cds=(217,1839) /gb=AF092132 /gi=5138913 /ug=Hs.284275 /len=4137	Hs.284275	p21 (CDKN1A)-activated kinase 2	PAK2

Hs.285176	0	88	577	**203164_at**	**203164_at**	7	1	0	0	0	0	350	941	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203164_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285176	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285176	Homo sapiens acetyl-Coenzyme A transporter (ACATN), mRNA /cds=(381,2030) /gb=NM_004733 /gi=6042194 /ug=Hs.285176 /len=2659	Hs.285176	acetyl-Coenzyme A transporter	ACATN

Hs.285932	0	89	578	**231846_at**	**231846_at**	2	0	0	0	0	12	406	1479	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231846_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285932	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285932	Homo sapiens hypothetical protein FLJ23322 (FLJ23322), mRNA /cds=(33,2087) /gb=NM_024955 /gi=13376440 /ug=Hs.285932 /len=3088	Hs.285932	hypothetical protein FLJ23322 FLJ23322

Hs.286218	0	90	579	**224097_s_at**	**224097_s_at**	12	6	5	0	0	0	442	307	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224097_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=286218	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=286218	Homo sapiens junctional adhesion molecule-1 mRNA, complete cds /cds=(146,1045) /gb=AF172398 /gi=13124448 /ug=Hs.286218 /len=3738	Hs.286218	junctional adhesion molecule 1 JAM1

Hs.28707	0	91	580	**222411_s_at**	**222411_s_at**	11	10	3	1	0	0	79	341	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222411_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28707	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28707	Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(56,613) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061	Hs.28707	signal sequence receptor, gamma (translocon-associated protein gamma)	SSR3

Hs.288932

0

92

581

222393_s_at

222393_s_at

10 9 6 1 0 4 29 272 3

1

1 at&chip_id=3 8932 8932 32 /len=3576

d=222393_s_ =Hs&CID=28 =Hs&CID=28 /ug=Hs.2889

pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=13376734

obeset_anno. v/UniGene/cl v/UniGene/cl 146

eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_025

bin/eike/prob http://www.nc http://www.nc 9)

gi-

metagen.de/c mRNA /cds=(300,80

http://intranet. (FLJ13194),

protein

FLJ13194

hypothetical

sapiens

Homo

hypothetical protein FLJ13194

FLJ13194

Hs.288932

Hs.289082	0	93	582	212737_at	212737_at	9	3	1	0	0	0	296	703	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212737_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289082	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289082	Homo sapiens GM2 ganglioside activator protein (GM2A), mRNA /cds=(95,676) /gb=NM_000405 /gi=16507969 /ug=Hs.289082 /len=2478	Hs.289082	GM2 ganglioside activator protein	GM2A

Hs.289114	0	94	583	**201645_at**	**201645_at**	7	5	4	2	1	3	1124	1050	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201645_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289114	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289114	Homo sapiens hexabrachion (tenascin C, cytotactin) (HXB), mRNA /cds=(313,6918) /gb=NM_002160 /gi=4504548 /ug=Hs.289114 /len=7560	Hs.289114	hexabrachion (tenascin C, cytotactin)	HXB

Hs.290070	0	95	584	**227958_s_at**	**227958_s_at**	0	0	0	0	0	14	356	1824	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=227958_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=290070	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=290070	Homo sapiens gelsolin (amyloidosis, Finnish type) (GSN), mRNA /cds=(14,2362) /gb=NM_000177 /gi=4504164 /ug=Hs.290070 /len=2602	Hs.290070	gelsolin (amyloidosis, Finnish type)	GSN

Hs.2913	0	96	585	**204600_at**	**204600_at**	5	4	4	1	0	9	562	485	2	1	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204600_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2913	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2913	Homo sapiens EphB3 (EPHB3), mRNA /cds=(27,3023) /gb=NM_004443 /gi=17975767 /ug=Hs.2913 /len=3805	Hs.2913	EphB3	EPHB3

Hs.298275	0	97	586	**220924_s_at**	**220924_s_at**	8	6	5	1	1	0	749	1003	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=220924_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=298275	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=298275	Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(533,1753) /gb=NM_018976 /gi=9506836 /ug=Hs.298275 /len=4384	Hs.298275	solute carrier family 38, member 2	SLC38A2
Hs.299883	0	98	587	**222692_s_at**	**222692_s_at**	8	1	0	0	0	0	409	1096	3	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222692_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=299883	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=299883	Homo sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769) /gb=NM_022763 /gi=12232434 /ug=Hs.299883 /len=2012	Hs.299883	hypothetical protein FLJ23399	FLJ23399

Hs.30212	0	99	588	**202467_s_at**	**202467_s_at**	11	3	2	0	0	0	376	648	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202467_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30212	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30212	Homo sapiens thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346) /gb=NM_004236 /gi=4759263 /ug=Hs.30212 /len=1951	Hs.30212	thyroid receptor interacting protein 15 TRIP15

Hs.302161

0

100

589

230464_at

230464_at

10 5 3 0 0 4 306 651 3 1 1 1

Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA /cds=(9,1205

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=3&chip_id=3 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30 http://www.ncbi.nlm.nih.gov/gb=NM_030760 /gi=18141314 /ug=Hs.3021 61 /len=2306

Hs.302161

endothelial differentiation, sphingolipid G-protein-coupled receptor, 8

EDG8

Hs.303125	0	101	590	**217744_s_at**	**217744_s_at**	10	7	7	1	0	0	540	381	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217744_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=303125	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=303125	Homo sapiens p53-induced protein PIGPC1 (PIGPC1), mRNA /cds=(72,653) /gb=NM_022121 /gi=11545842 /ug=Hs.303125 /len=1098	Hs.303125	p53-induced protein PIGPC1	PIGPC1

Hs.306098	0	102	591	**216594_x_at**	**216594_x_at**	7	4	1	0	0	0	667	545	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=216594_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=306098	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=306098	Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA /cds=(6,977) /gb=NM_001353 /gi=5453542 /ug=Hs.306098 /len=1207	Hs.306098	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	AKR1C1

Hs.306189	0	103	592	**224634_at**	**224634_at**	4	0	0	0	0	0	252	1268	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224634_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=306189	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=306189	Homo sapiens DKFZP434F1735 protein (DKFZP434F1735), mRNA /cds=(1164,1583) /gb=NM_015590 /gi=7661571 /ug=Hs.306189 /len=2106	Hs.306189	DKFZP434F1735 protein	DKFZP434F1735
Hs.30738	0	104	593	**234672_s_at**	**234672_s_at**	7	3	0	0	0	0	302	1064	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=234672_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30738	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30738	Novel human gene mapping to chomosome 1 /cds=(174,2195) /gb=AL354613 /gi=7688173 /ug=Hs.30738 /len=4706	Hs.30738	hypothetical protein FLJ10407	FLJ10407

Hs.313	0	105	594	**209875_s_at**	**209875_s_at**	12	10	10	6	1	0	610	105	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209875_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=313	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=313	Homo sapiens secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA /cds=(87,989) /gb=NM_000582 /gi=4759165 /ug=Hs.313 /len=1524	Hs.313	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	SPP1

Hs.31386	0	106	595	**223122_s_at**	**223122_s_at**	5	4	4	1	1	5	961	1741	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223122_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31386	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31386	Homo sapiens pancreas tumor-related protein (FKSG12) mRNA, complete cds /cds=(237,1124) /gb=AF311912 /gi=10946502 /ug=Hs.31386 /len=1988

Hs.31386 [illegible] 5, clone MGC:9395 IMAGE:3874262, mRNA, complete cds

Hs.323494	0	107	596	**243643_x_at**	**243643_x_at**	8	2	0	0	0	6	415	871	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=243643_x_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323494	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323494	Homo sapiens cDNA FLJ31101 fis, clone IMR321000266, weakly similar to ZINC/CADMIUM RESISTANCE PROTEIN /cds=(37,1422) /gb=AK055663 /gi=16550445 /ug=Hs.323494 /len=2450	Hs.323494	Homo sapiens cDNA FLJ31101 fis, clone IMR321000266, weakly similar to ZINC/CADMIUM RESISTANCE PROTEIN

Hs.323733	0	108	597	**223278_at**	**223278_at**	12	12	12	6	0	1	447	19	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223278_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323733	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323733	Homo sapiens connexin 26 (GJB2) mRNA, complete cds /cds=(198,878) /gb=M86849 /gi=4481752 /ug=Hs.323733 /len=2311	Hs.323733	gap junction protein, beta 2, 26kD (connexin 26) GJB2

Hs.32603	0	109	598	**219873_at**	**219873_at**	10	8	7	2	0	3	646	247	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219873_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=32603	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=32603	Homo sapiens hypothetical protein MGC3279 similar to collectins (MGC3279), mRNA /cds=(82,897) /gb=NM_024027 /gi=13128971 /ug=Hs.32603 /len=1257	Hs.32603	hypothetical protein MGC3279 similar to collectins MGC3279

Hs.32949	0	110	599	**210397_at**	**210397_at**	5	5	5	0	3	4	1099	1666	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210397_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=32949	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=32949	Homo sapiens defensin, beta 1 (DEFB1), mRNA /cds=(71,277) /gb=NM_005218 /gi=13124884 /ug=Hs.32949 /len=366	Hs.32949	defensin, beta 1	DEFB1

Hs.334437	0	111	600	**224435_at**	**224435_at**	8	6	0	0	0	0	411	803	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224435_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334437	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334437	Homo sapiens hypothetical protein MGC4248 (MGC4248), mRNA /cds=(70,720) /gb=NM_032333 /gi=14150115 /ug=Hs.334437 /len=1278	Hs.334437

Hs.339826	0	112	601	231948_s_at	231948_s_at	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.339826	0	112,2	601,2	**231948_s_at**	**231948_s_at**	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.339826	0	112,3	601,3	**231948_s_at**	**231948_s_at**	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.339826	0	112,4	601,4	**231948_s_at**	**231948_s_at**	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826

Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.339826	0	112,5	601,5	**231948_s_at**	**231948_s_at**	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3 9826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.339826	0	112,6	601,6	**231948_s_at**	**231948_s_at**	6	5	0	0	0	1	282	791	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231948_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=339826	Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) /cds=UNKNOWN /gb=AK023919 /gi=10436004 /ug=Hs.339826 /len=2152	Hs.339826

Hs.349177	0	113	602	**225359_at**	**225359_at**	9	3	1	0	0	0	184	748	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225359_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349177	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349177	Homo sapiens, Similar to RIKEN cDNA 1810055D05 gene, clone MGC:9296 IMAGE:3892297, mRNA, complete cds /cds=(124,474) /gb=BC009702 /gi=16307226 /ug=Hs.349177 /len=580	Hs.349177
Hs.349204	0	114	603	**223869_at**	**223869_at**	6	6	5	5	0	8	744	1043	3		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223869_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349204	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349204	Homo sapiens sclerostin (SOST), mRNA /cds=(47,688) /gb=NM_025237 /gi=13376845 /ug=Hs.349204 /len=2323	Hs.349204

Hs.351875	0	115	604	**201754_at**	**201754_at**	10	3	0	0	0	0	159	780	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201754_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351875	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351875	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA /cds=(60,287) /gb=NM_004374 /gi=17999531 /ug=Hs.351875 /len=444	Hs.351875	
Hs.36793	0	116	605	**219874_at**	**219874_at**	9	5	5	0	0	2	466	597	2	1			1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219874_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=36793	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=36793	Homo sapiens hypothetical protein FLJ23188 (FLJ23188), mRNA /cds=(665,1591) /gb=NM_024628 /gi=13375853 /ug=Hs.36793 /len=2349	Hs.36793	(potassium/chloride transporters), member 8 SLC12A8

nudix (nucleoside diphosphate linked moiety X)-type motif 1
NUDT1

Hs.388

Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), mRNA /cds=(26,496 /gb=NM_002452 /gi=4505274 /ug=Hs.388 /len=643

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204766_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=38

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=38

8

1 1

2

270

52 0 0 0 0 0 6 9 13

204766_s_at

204766_s_at

606

117

0

Hs.388

Hs.41690	0	118	607	**206032_at**	**206032_at**	13	12	12	7	1	0	698	46	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206032_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41690	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41690	Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA /cds=(63,2582) /gb=NM_024423 /gi=13435368 /ug=Hs.41690 /len=5920	Hs.41690	desmocollin 3	DSC3

Hs.44

0

119

608

211737_x_at

211737_x_at

211737_x_at

6 9

8

6

3

1 2

2

922

414

2 1

1 1

at&chip_id=2 =Hs&CID=44 /len=2657

d=211737_x_ ust.cgi?ORG /ug=Hs.44

pl?probeset_i v/UniGene/cl /gi=4506280

obeset_anno. bi.nlm.nih.go 825

eset_anno/pr http://www.nc /gb=NM_002

bin/eike/prob 047)

gi- /cds=(1541,2

metagen.de/c mRNA

http://intranet. (PTN),

factor 1)

promoting

8, neurite

growth factor

binding

(heparin

pleiotrophin

sapiens

Homo

Hs.44

pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)

PTN

Hs.48956	0	120	609	**231771_at**	**231771_at**	13	12	12	11	0	1	262	2	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=231771_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=48956	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=48956	Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), mRNA /cds=(0,785) /gb=NM_006783 /gi=5803020 /ug=Hs.48956 /len=786	Hs.48956	gap junction protein, beta 6 (connexin 30) GJB6
Hs.48998	0	121	610	**204359_at**	**204359_at**	8	8	6	1	0	1	504	211	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204359_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=48998	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=48998	Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA /cds=(1124,3106) /gb=NM_013231 /gi=7019380 /ug=Hs.48998 /len=7527	Hs.48998	fibronectin leucine rich transmembrane protein 2 FLRT2

Hs.5338

0
123
612
203963_at
203963_at
1011
1575
2 1
1 1

7 5 4 2 3 1 0 0 0 2 166 3 1 1 1

Homo sapiens carbonic anhydrase XII (CA12), mRNA /cds=(115,11 79)

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=203963_at&chip_id=2 38

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=53 38

bi.nlm.nih.gov/gb=NM_001218 /gi=9951924 /ug=Hs.5338 /len=2775

carbonic anhydrase XII CA12

Hs.5243

0
122
611
223193_x_at
223193_x_at
13 11 9 0 0 0 0 2 166 3 1 1 1

Homo sapiens hypothetical protein, estradiol-induced (E2IG5), mRNA /cds=(53,499)

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=223193_x_at&chip_id=3 43

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=52 43

http://www.ncbi.nlm.nih.gov/gb=NM_014367 /gi=7657049 /ug=Hs.5243 /len=800

hypothetical protein, estradiol-induced E2IG5

Hs.55279	0	124	613	**204855_at**	**204855_at**	11	7	6	3	1	0	733	111	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204855_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=55279	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=55279	Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 (SERPINB5), mRNA /cds=(75,1202) /gb=NM_002639 /gi=4505788 /ug=Hs.55279 /len=2566	Hs.55279	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 SERPINB5

Hs.57101	0	125	614	**202107_s_at**	**202107_s_at**	10	10	9	4	0	0	187	170	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202107_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=57101	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=57101	Homo sapiens MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) (MCM2), mRNA /cds=(30,2708) /gb=NM_004526 /gi=4758705 /ug=Hs.57101 /len=3379	Hs.57101	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	MCM2

Hs.58561	0	126	615	219936_s_at	219936_s_at	12	10	7	4	1	0	473	207	2	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219936_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=58561	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=58561	Homo sapiens G protein-coupled receptor 87 (GPR87), mRNA /cds=(249,1325) /gb=NM_023915 /gi=13236505 /ug=Hs.58561 /len=1402	Hs.58561	G protein-coupled receptor 87 GPR87
Hs.5943	0	127	616	222730_s_at	222730_s_at	8	2	0	0	0	1	324	1011	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222730_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5943	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5943	Homo sapiens rec (LOC51201), mRNA /cds=(397,1500) /gb=NM_016353 /gi=7705948 /ug=Hs.5943 /len=3322	Hs.5943	zinc finger, DHHC domain containing 2 ZDHHC2

Hs.63788	0	128	617	**212694_s_at**	**212694_s_at**	11	8	5	0	0	0	65	460	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212694_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=63788	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=63788	Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA /cds=(0,1619) /gb=NM_000532 /gi=4557043 /ug=Hs.63788 /len=1620	Hs.63788	propionyl Coenzyme A carboxylase, beta polypeptide	PCCB

Hs.69469	0	129	618	202232_s_at	202232_s_at	10	8	7	0	1	0	760	458	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202232_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69469	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69469	Homo sapiens dendritic cell protein (GA17), mRNA /cds=(51,1175) /gb=NM_006360 /gi=5453653 /ug=Hs.69469 /len=1249	Hs.69469	dendritic cell protein	GA17
Hs.69517	0	130	619	223687_s_at	223687_s_at	9	8	6	2	1	4	686	441	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223687_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69517	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69517	Homo sapiens, clone MGC:5257 IMAGE:3457263, mRNA, complete cds /cds=(43,540) /gb=BC001291 /gi=12654892 /ug=Hs.69517 /len=1373	Hs.69517	cDNA for differentially expressed CO16 gene	HSJ001348

DCK	deoxycytidine kinase	Hs.709	Homo sapiens deoxycytidine kinase (DCK), mRNA /cds=(159,941) /gb=NM_000788 /gi=4503268 /ug=Hs.709 /len=2460	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=709	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=709	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203302_at&chip_id=2	1	1	2	367	583	0	1	2	6	9	9	203302_at	203302_at	620	131	0	Hs.709
DC42	hypothetical protein DC42	Hs.72805	Homo sapiens cDNA: FLJ22093 fis, clone HEP16739 /cds=UNKNOWN /gb=AK025746 /gi=10438358 /ug=Hs.72805 /len=2294	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=72805	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=72805	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223013_at&chip_id=3	1	1	3	1188	399	0	0	0	1	1	5	223013_at	223013_at	621	132	0	Hs.72805

Hs.7327	0	133	622	**218182_s_at**	**218182_s_at**	10	7	5	1	1	2	623	303	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218182_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7327	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7327	Homo sapiens senescence-associated epithelial membrane protein (SEMP1) mRNA, complete cds /cds=(220,855) /gb=AF101051 /gi=4323580 /ug=Hs.7327 /len=3443	Hs.7327	claudin 1	CLDN1

Hs.74376	0	134	623	213131_at	213131_at	10	10	8	5	1	2	983	106	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213131_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74376	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74376	Homo sapiens olfactomedin 1 (OLFM1), transcript variant 1, mRNA /cds=(285,1688) /gb=NM_014279 /gi=17136142 /ug=Hs.74376 /len=2741	Hs.74376	olfactomedin 1	OLFM1

Hs.74619	0	135	624	**200830_at**	**200830_at**	13	9	4	0	0	0	43	379	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200830_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74619	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74619	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (PSMD2), mRNA /cds=(112,2673) /gb=NM_002808 /gi=4506226 /ug=Hs.74619 /len=2828	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 PSMD2

Hs.75187	0	136	625	**212773_s_at**	**212773_s_at**	11	6	3	0	0	0	428	522	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212773_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75187	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75187	Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) homolog (KIAA0016), mRNA /cds=(101,538) /gb=NM_014765 /gi=7657256 /ug=Hs.75187 /len=3259	Hs.75187	translocase of outer mitochondrial membrane 20 (yeast) homolog	TOMM20-PENDING

Hs.75231	0	137	626	**209900_s_at**	**209900_s_at**	12	11	10	5	0	1	500	67	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209900_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75231	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75231	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA /cds=(12,1514) /gb=NM_003051 /gi=4506982 /ug=Hs.75231 /len=2578	Hs.75231	solute carrier family 16 (monocarboxylic acid transporters), member 1	SLC16A1

Hs.75939	0	138	627	**209825_s_at**	**209825_s_at**	10	5	4	0	0	4	129	600	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209825_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75939	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75939	Homo sapiens uridine monophosphate kinase (UMPK), mRNA /cds=(218,553) /gb=NM_012474 /gi=6912739 /ug=Hs.75939 /len=831	Hs.75939	uridine monophosphate kinase UMPK

Hs.76136	0	139	628	**208864_s_at**	**208864_s_at**	8	7	5	0	1	0	917	526	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208864_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76136	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76136	Homo sapiens thioredoxin (TXN), mRNA /cds=(63,380) /gb=NM_003329 /gi=4507744 /ug=Hs.76136 /len=501	Hs.76136	thioredoxin TXN

Hs.77254	0	140	629	**201518_at**	**201518_at**	11	5	4	0	0	0	436	383	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201518_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77254	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77254	Homo sapiens chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1), mRNA /cds=(216,773) /gb=NM_006807 /gi=5803075 /ug=Hs.77254 /len=2148	Hs.77254

chromobox homolog 1 (HP1 beta homolog Drosophila)

CBX1

Hs.77329	0	141	630	**201433_s_at**	**201433_s_at**	11	10	7	1	0	0	58	284	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201433_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77329	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77329	Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA /cds=(102,1523) /gb=NM_014754 /gi=7662646 /ug=Hs.77329 /len=2504	Hs.77329	phosphatidylserine synthase 1	PTDSS1

Hs.77356	0	142	631	207332_s_at	207332_s_at	13	11	8	1	0	0	92	154	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=207332_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77356	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77356	Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA /cds=(263,2545) /gb=NM_003234 /gi=4507456 /ug=Hs.77356 /len=5010	Hs.77356	transferrin receptor (p90, CD71)	TFRC

Hs.77422	0	143	632	**201136_at**	**201136_at**	8	5	5	1	1	0	894	726	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201136_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77422	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77422	Homo sapiens proteolipid protein 2 (colonic epithelium-enriched) (PLP2), mRNA /cds=(75,533) /gb=NM_002668 /gi=4505892 /ug=Hs.77422 /len=945	Hs.77422	proteolipid protein 2 (colonic epithelium-enriched)	PLP2

Hs.78802	0	144	633	**209945_s_at**	**209945_s_at**	7	6	4	0	0	0	394	536	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209945_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78802	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78802	Homo sapiens glycogen synthase kinase 3 beta (GSK3B), mRNA /cds=(39,1301) /gb=NM_002093 /gi=4504162 /ug=Hs.78802 /len=1389	Hs.78802	glycogen synthase kinase 3 beta GSK3B

Hs.78867	0	145	634	**204469_at**	**204469_at**	8	6	4	3	4	0	826	541	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204469_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78867	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78867	Homo sapiens protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(147,7091) /gb=NM_002851 /gi=4506328 /ug=Hs.78867 /len=7941	Hs.78867	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	PTPRZ1

Hs.79006	0	146	635	**203270_at**	**203270_at**	5	0	0	0	0	8	84	1070	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203270_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79006	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79006	Homo sapiens deoxythymidylate kinase (thymidylate kinase) (DTYMK), mRNA /cds=(27,662) /gb=NM_012145 /gi=6912339 /ug=Hs.79006 /len=1000	Hs.79006	deoxythymidylate kinase (thymidylate kinase)	DTYMK

Hs.7912	0	147	636	**204105_s_at**	**204105_s_at**	11	8	6	3	0	3	308	293	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204105_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7912	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7912	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA /cds=(414,3956) /gb=NM_005010 /gi=4826863 /ug=Hs.7912 /len=6218	Hs.7912	neuronal cell adhesion molecule	NRCAM

Hs.79432	0	148	637	**203184_at**	**203184_at**	6	5	5	4	0	4	839	780	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203184_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79432	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79432	Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA /cds=(0,8735) /gb=NM_001999 /gi=4755135 /ug=Hs.79432 /len=10166	Hs.79432	fibrillin 2 (congenital contractural arachnodactyly) FBN2

Hs.79748	0	149	638	**200924_s_at**	**200924_s_at**	3	0	0	0	0	8	305	1423	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200924_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79748	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79748	Homo sapiens solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2), mRNA /cds=(138,1727) /gb=NM_002394 /gi=4505140 /ug=Hs.79748 /len=1861	Hs.79748	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	SLC3A2

Hs.7980	0	150	639	224452_s_at	224452_s_at	11	8	2	0	0	1	77	402	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224452_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7980	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7980	Homo sapiens hypothetical protein MGC12966 (MGC12966), mRNA /cds=(201,407) /gb=NM_032706 /gi=14249303 /ug=Hs.7980 /len=2221	Hs.7980	hypothetical protein MGC12966 MGC12966

Hs.80986	0	151	640	**208972_s_at**	**208972_s_at**	9	7	3	0	0	0	260	729	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208972_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80986	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80986	Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(119,529) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631	Hs.80986	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	ATP5G1

Hs.81134	0	152	641	**212657_s_at**	**212657_s_at**	12	11	8	5	0	0	467	128	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212657_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81134	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81134	H.sapiens mRNA for interleukin-1 receptor antagonist antagonist /cds=(23,556) /gb=X52015 /gi=32576 /ug=Hs.81134 /len=1740	Hs.81134	interleukin 1 receptor antagonist IL1RN

Hs.82109	0	153	642	**201287_s_at**	**201287_s_at**	9	4	4	0	0	0	625	402	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201287_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82109	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82109	Homo sapiens syndecan 1 (SDC1), mRNA /cds=(205,1137) /gb=NM_002997 /gi=4506858 /ug=Hs.82109 /len=2402

Hs.82109 syndecan 1 SDC1

Hs.82587	0	154	643	**215724_at**	**215724_at**	8	5	3	1	0	6	559	357	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215724_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82587	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82587	Homo sapiens phospholipase D1, phophatidylcholine-specific (PLD1), mRNA /cds=(95,3319) /gb=NM_002662 /gi=4505872 /ug=Hs.82587 /len=3609	Hs.82587	phospholipase D1, phophatidylcholine-specific	PLD1

Hs.8262	0	155	644	**200821_at**	**200821_at**	10	6	2	0	1	0	345	579	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200821_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8262	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8262	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA /cds=(137,1369) /gb=NM_013995 /gi=7669502 /ug=Hs.8262 /len=4006	Hs.8262	lysosomal-associated membrane protein 2	LAMP2

Hs.85201	0	156	645	**209732_at**	**209732_at**	6	4	4	3	1	0	894	1260	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209732_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=85201	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=85201	Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) (CLECSF2), mRNA /cds=(132,581) /gb=NM_005127 /gi=4826676 /ug=Hs.85201 /len=759	Hs.85201	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	CLECSF2

Hs.85701
0
157
646
204369_at
204369_at
8 2 1 0 0 5 402 835 2 1
1
http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info?probeset_id=2&chip_id=2 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=85701 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=85701 /gb=NM_006218 /gi=5453891 /ug=Hs.85701 /len=3424
Homo sapiens phosphoinositide-3-kinase, catalytic, alpha polypeptide (PIK3CA), mRNA /cds=(12,3218)
Hs.85701
phosphoinositide-3-kinase, catalytic, alpha polypeptide
PIK3CA

Hs.87417	0	158	647	**210074_at**	**210074_at**	11	10	8	.5	1	2	487	93	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210074_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=87417	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=87417	Homo sapiens cathepsin L2 (CTSL2), mRNA /cds=(69,1073) /gb=NM_001333 /gi=4503152 /ug=Hs.87417 /len=1342	Hs.87417	cathepsin L2 CTSL2

Hs.8786	0	159	648	203921_at	203921_at	8	7	5	2	0	4	815	218	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203921_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8786	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8786	Homo sapiens mRNA for N-acetylglucosamine 6-O-sulfotransferase, complete cds /cds=(1525,2976) /gb=AB021124 /gi=10944289 /ug=Hs.8786 /len=3535	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	CHST2

Hs.89306	0	160	649	**219650_at**	**219650_at**	10	9	4	0	0	3	24	390	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219650_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89306	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89306	Homo sapiens cDNA FLJ31932 fis, clone NT2RP7006296, weakly similar to EXCISION REPAIR PROTEIN ERCC-6 /cds=UNKNOWN /gb=AK056494 /gi=16551910 /ug=Hs.89306 /len=4334	Hs.89306	hypothetical protein FLJ20105	FLJ20105

ATP-binding cassette, sub-family C (CFTR/MRP), member 1

ABCC1

Hs.89433

Hs.89433	0	161	650	**202804_at**	**202804_at**	10	8	5	0	0	0	531	631	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202804_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89433	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89433	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791) /gb=NM_004996 /gi=9955961 /ug=Hs.89433 /len=5927

Hs.89626	0	162	651	**211756_at**	**211756_at**	11	11	11	10	0	2	415	1	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211756_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89626	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89626	Homo sapiens parathyroid hormone-like hormone (PTHLH), mRNA /cds=(303,830) /gb=NM_002820 /gi=4506268 /ug=Hs.89626 /len=1595	Hs.89626	parathyroid hormone-like hormone	PTHLH

Hs.90744	0	163	652	208777_s_at	208777_s_at	9	4	2	0	0	1	390	714	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208777_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90744	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90744	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268) /gb=NM_002815 /gi=4506218 /ug=Hs.90744 /len=1269	Hs.90744	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	PSMD11
Hs.91143	0	164	653	216268_s_at	216268_s_at	10	6	3	0	1	0	734	373	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=216268_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=91143	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=91143	Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA /cds=(413,4069) /gb=NM_000214 /gi=4557678 /ug=Hs.91143 /len=5896	Hs.91143	jagged 1 (Alagille syndrome)	JAG1

Hs.93002	0	165	654	**202954_at**	**202954_at**	7	5	1	0	0	1	333	1124	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202954_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=93002	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=93002	Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), mRNA /cds=(40,579) /gb=NM_007019 /gi=5902145 /ug=Hs.93002 /len=783	Hs.93002	ubiquitin-conjugating enzyme E2C	UBE2C

Hs.94560	0	166	655	**217901_at**	**217901_at**	10	6	4	1	1	0	417	366	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217901_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=94560	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=94560	Homo sapiens desmoglein 2 (DSG2), mRNA /cds=(11,3364) /gb=NM_001943 /gi=4503402 /ug=Hs.94560 /len=3516	Hs.94560

Hs.95577	0	167	656	**202246_s_at**	**202246_s_at**	11	8	5	1	0	0	413	300	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202246_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=95577	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=95577	Homo sapiens cyclin-dependent kinase 4 (CDK4), transcript variant 1, mRNA /cds=(227,1138) /gb=NM_000075 /gi=16936531 /ug=Hs.95577 /len=1474	Hs.95577	cyclin-dependent kinase 4 CDK4

Ric-like, expressed in many tissues (Drosophila)
RIT

Hs.96038

Homo sapiens Ric-like, expressed in many tissues (Drosophila) (RIT), mRNA /cds=(135,794)

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=2&chip_id=2 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=96038 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=96038 /gb=NM_006912 /gi=5902049 /ug=Hs.96038 /len=1037

Hs.96038
0
168
657
209882_at
209882_at
10 9 6 3 0 1 468 233 2 1 1

Hs.9914	0	169	658	**204948_s_at**	**204948_s_at**	11	8	7	2	0	2	682	186	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204948_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9914	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9914	Homo sapiens follistatin (FST), transcript variant FST317, mRNA /cds=(27,980) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386	Hs.9914	follistatin FST
	0	170	659	**229900_at**	**229900_at**	9	7	5	1	1	2	896	587	3	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=229900_at&chip_id=3					CD109

	0	171	660	**225787_at**	**225787_at**	6	0	0	0	0	2	357	1191	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225787_at&chip_id=3				
	1	172	661	**213535_s_at**	**213535_s_at**	6	0	0	0	0	0	220	808	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213535_s_at&chip_id=2				
Hs.104741	1	173	662	**219148_at**	**219148_at**	12	11	8	1	0	1	85	147	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219148_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104741	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104741	Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA /cds=(201,1169) /gb=NM_018492 /gi=18490990 /ug=Hs.104741 /len=1899	Hs.104741	T-LAK cell-originated protein kinase TOPK

Hs.105097	1	174	663	202338_at	202338_at	12	9	7	0	0	1	35	172	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202338_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=105097	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=105097	Homo sapiens thymidine kinase 1, soluble (TK1), mRNA /cds=(57,761) /gb=NM_003258 /gi=4507518 /ug=Hs.105097 /len=1421	Hs.105097	thymidine kinase 1, soluble	TK1

Hs.106242

1

175

664

206515_at

206515_at

206515_at

8 7 6 5 0 5 743 72 2 1

1 1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=2&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106242

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106242

6242 6242

Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA /cds=(50,1612) /gb=NM_000896 /gi=4503240 /ug=Hs.106242 42 /len=5050

Hs.106242

cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) CYP4F3

Hs.107707	1	176	665	**226296_s_at**	**226296_s_at**	9	4	3	0	0	0	214	640	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=226296_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=107707	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=107707	Homo sapiens mitochondrial ribosomal protein S15 (MRPS15), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,866) /gb=NM_031280 /gi=16554610 /ug=Hs.107707 /len=891	Hs.107707	mitochondrial ribosomal protein S15	MRPS15

Hs.108106	1	177	666	**225655_at**	**225655_at**	10	5	3	0	0	4	168	581	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225655_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108106	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108106	Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), mRNA /cds=(84,2465) /gb=NM_013282 /gi=16507203 /ug=Hs.108106 /len=3828	Hs.108106	ubiquitin-like, containing PHD and RING finger domains, 1	UHRF1

RAN, member RAS oncogene family

RAN

Hs.10842

Homo sapiens RAN, member RAS oncogene family (RAN), mRNA /cds=(114,764)

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200750_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=10842

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=10842

http://www.ncbi.nlm.nih.gov/gb=NM_006325

/gi=6042206

/ug=Hs.10842

2 /len=1656

1

1

2

86

190

0

1

2

8

10

11

200750_s_at

200750_s_at

667

178

1

Hs.10842

Hs.108854	1	179	668	**218728_s_at**	**218728_s_at**	12	8	5	2	1	0	515	404	2	1		1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218728_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108854	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=108854	Homo sapiens cDNA: FLJ20916 fis, clone ADSE00738, highly similar to AF161512 Homo sapiens HSPC163 mRNA /cds=UNKNOWN /gb=AK024569 /gi=10436879 /ug=Hs.108854 /len=2233	Hs.108854	HSPC163 protein	HSPC163
Hs.109494	1	180	669	**218407_x_at**	**218407_x_at**	2	0	0	0	0	12	359	1387	2		1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218407_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=109494	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=109494	Homo sapiens secreted protein of unknown function (SPUF), mRNA /cds=(60,578) /gb=NM_013349 /gi=7019544 /ug=Hs.109494 /len=724	Hs.109494	secreted protein of unknown function	SPUF

Hs.111779	1	181	670	**200665_s_at**	**200665_s_at**	8	8	7	2	1	2	833	564	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200665_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=111779	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=111779	Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA /cds=(57,968) /gb=NM_003118 /gi=4507170 /ug=Hs.111779 /len=2133	Hs.111779	secreted protein, acidic, cysteine-rich (osteonectin)	SPARC

Hs.116724	1	182	671	**206561_s_at**	**206561_s_at**	12	11	11	10	1	1	549	5	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206561_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=116724	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=116724	Homo sapiens aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA /cds=(39,989) /gb=NM_020299 /gi=13346507 /ug=Hs.116724 /len=1316	Hs.116724	aldo-keto reductase family 1, member B10 (aldose reductase)	AKR1B10

Hs.118638	1	183	672	**201577_at**	**201577_at**	14	13	13	3	0	0	13	97	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201577_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=118638	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=118638	Homo sapiens non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(84,542) /gb=NM_000269 /gi=4557796 /ug=Hs.118638 /len=732	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	NME1

Hs.118778

Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDELR2), mRNA /cds=(12,650

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=200700_s_at&chip_id=2 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11)

/gb=NM_006854 /gi=8051609 /ug=Hs.11878 78 /len=1153

1 8778

200700_s_at 11 8 4 2 1 0 621 275 2 1

200700_s_at 673

184

1

Hs.118778

SCD

stearoyl-CoA desaturase (delta-9-desaturase)

Hs.119597

Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds /cds=(380,14 gi-

http://intranet.metagen.de/cbin/elike/probeset_anno/probeset_anno.pl?probeset_id=200832_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/ust.cgi?ORG=Hs&CID=11

http://www.ncbi.nlm.nih.gov/UniGene/ust.cgi?ORG=Hs&CID=11

9597

59)

/gb=AB03226 1

/gi=7415720 /ug=Hs.1195 97 /len=5329

Hs.119597

1

185

674

200832_s_at

200832_s_at

12 11 9 4 1 0 516 86 2 1

1

Hs.12677	1	186	675	**218732_at**	**218732_at**	10	3	1	0	1	0	345	738	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218732_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=12677	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=12677	Homo sapiens cDNA FLJ32471 fis, clone SKNMC2000322, weakly similar to MAJOR CENTROMERE AUTOANTIGEN B /cds=(350,1090) /gb=AK057033 /gi=16552603 /ug=Hs.12677 /len=2047	Hs.12677	CGI-147 protein	LOC51651

Homo sapiens cDNA FLJ30755 fis, clone FEBRA2000452

Hs.132554

http://intranet.metagen.de/cgi-bin/eike/probeset_annotation.pl?probeset_id=238029_s_at&chip_id=3

Homo sapiens cDNA FLJ30794 fis, clone FEBRA2001093, weakly similar to MONOCARBOXYLATE TRANSPORTER 4 /cds=(238,1248) /gb=AK055356 /gi=16550678 /ug=Hs.132554 /len=3645

Hs.132554

1

187

676

238029_s_at

238029_s_at

238029_s_at

9 6 6 2 1 2 732 271 3 1

1

Hs.14732

1

188

677

204058_at

204058_at

204058_at

8 7 7 3 2 0 595 100 2

1

1 &chip_id=2 732

d=204058_at =Hs&CID=14 732 2 /len=2212

pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=13435400

obeset_anno. v/UniGene/cl v/UniGene/cl 395

eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_002

bin/eike/prob http://www.nc http://www.nc 25)

gi-

metagen.de/c

http://intranet.

/cds=(107,18

mRNA

(ME1),

cytosolic

dependent,

NADP(+)-

enzyme 1,

sapiens malic

Homo

malic enzyme 1, NADP(+)-dependent, cytosolic

ME1

Hs.14732

Hs.151738	1	189	678	**203936_s_at**	**203936_s_at**	6	4	4	3	0	2	739	925	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203936_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=151738	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=151738	Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA /cds=(19,2142) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	MMP9

Hs.155462	1	190	679	**201930_at**	**201930_at**	13	11	8	1	0	0	11	167	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201930_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155462	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155462	Homo sapiens MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (MCM6), mRNA /cds=(61,2526) /gb=NM_005915 /gi=7427518 /ug=Hs.155462 /len=2917	Hs.155462	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	MCM6

Hs.155485	1	191	680	**202347_s_at**	**202347_s_at**	10	7	5	0	1	0	677	517	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202347_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155485	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155485	Homo sapiens huntingtin interacting protein 2 (HIP2), mRNA /cds=(77,679) /gb=NM_005339 /gi=12545382 /ug=Hs.155485 /len=2223	Hs.155485	huntingtin interacting protein 2 HIP2

Hs.1634	1	192	681	**204695_at**	**204695_at**	0	0	0	0	0	14	34	437	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204695_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1634	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1634	Homo sapiens cell division cycle 25A (CDC25A), mRNA /cds=(459,2030) /gb=NM_001789 /gi=4502704 /ug=Hs.1634 /len=2419	Hs.1634	cell division cycle 25A	CDC25A

Hs.1695	1	193	682	**204580_at**	**204580_at**	11	10	9	7	0	1	670	41	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204580_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1695	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1695	Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA /cds=(12,1424) /gb=NM_002426 /gi=4505206 /ug=Hs.1695 /len=1778	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	MMP12

Hs.169756	1	194	683	**208747_s_at**	**208747_s_at**	9	5	5	2	1	0	802	238	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208747_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169756	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169756	Homo sapiens complement component 1, s subcomponent (C1S), mRNA /cds=(202,2268) /gb=NM_001734 /gi=4502494 /ug=Hs.169756 /len=2647	Hs.169756	complement component 1, s subcomponent	C1S

Hs.169840	1	195	684	**204822_at**	**204822_at**	12	9	5	1	0	1	381	251	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204822_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169840	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169840	Homo sapiens TTK protein kinase (TTK), mRNA /cds=(1025,3550) /gb=NM_003318 /gi=4507718 /ug=Hs.169840 /len=3866	Hs.169840	TTK protein kinase TTK

Hs.178655	1	196	685	**218497_s_at**	**218497_s_at**	12	11	11	0	0	0	18	178	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218497_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=178655	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=178655	Homo sapiens ribonuclease H1 (RNASEH1), mRNA /cds=(61,921) /gb=NM_002936 /gi=4506554 /ug=Hs.178655 /len=1147	Hs.178655	ribonuclease H1 RNASEH1

Hs.178695	1	197	686	**210059_s_at**	**210059_s_at**	7	6	3	0	0	1	540	433	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210059_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=178695	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=178695	Homo sapiens mitogen-activated protein kinase 13 (MAPK13), mRNA /cds=(22,1119) /gb=NM_002754 /gi=4506084 /ug=Hs.178695 /len=1259	Hs.178695	mitogen-activated protein kinase 13	MAPK13

Hs.181309	1	198	687	**201317_s_at**	**201317_s_at**	9	6	4	0	2	0	529	404	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201317_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=181309	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=181309	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA /cds=(0,704) /gb=NM_002787 /gi=4506180 /ug=Hs.181309 /len=866	Hs.181309	proteasome (prosome, macropain) subunit, alpha type, 2 PSMA2

Hs.182018	1	199	688	**201587_s_at**	**201587_s_at**	7	2	1	0	0	0	277	1041	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201587_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182018	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182018	Homo sapiens interleukin-1 receptor-associated kinase 1 (IRAK1), mRNA /cds=(79,2217) /gb=NM_001569 /gi=4755143 /ug=Hs.182018 /len=3583	Hs.182018	interleukin-1 receptor-associated kinase 1	IRAK1

Hs.184062	1	200	689	**224376_s_at**	**224376_s_at**	13	12	9	1	0	0	28	91	3	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224376_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184062	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184062	Homo sapiens putative Rab5-interacting protein (RIP5), mRNA /cds=(182,571) /gb=NM_018840 /gi=10047115 /ug=Hs.184062 /len=1104	Hs.184062	chromosome 20 open reading frame 24	C20orf24
Hs.184339	1	201	690	**204825_at**	**204825_at**	13	12	11	4	0	0	61	81	2		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204825_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184339	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184339	Homo sapiens likely ortholog of maternal embryonic leucine zipper kinase (KIAA0175), mRNA /cds=(170,2125) /gb=NM_014791 /gi=7661973 /ug=Hs.184339 /len=2470	Hs.184339	likely ortholog of maternal embryonic leucine zipper kinase	MELK

Hs.184601

1

202

691

201195_s_at

201195_s_at

201195_s_at

10 10 8 4 0 4 437 135 2 1

1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=201195_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184601

4601

Homo sapiens L-type amino acid transporter subunit LAT1 mRNA, complete cds /cds=(66,1589) /gb=AF104039 /gi=4426639 /ug=Hs.184601 Hs.184601

solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 SLC7A5

Hs.194698	1	203	692	**202705_at**	**202705_at**	13	13	13	4	0	0	111	65	2		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202705_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194698	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194698	Homo sapiens cyclin B2 (CCNB2), mRNA /cds=(148,1344) /gb=NM_004701 /gi=10938017 /ug=Hs.194698 /len=1530	Hs.194698	cyclin B2	CCNB2
Hs.19554	1	204	693	**203550_s_at**	**203550_s_at**	3	0	0	0	0	7	385	1223	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203550_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=19554	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=19554	Homo sapiens chromosome 1 open reading frame 2 (C1orf2), mRNA /cds=(578,2587) /gb=NM_006589 /gi=5729751 /ug=Hs.19554 /len=3152	Hs.19554	chromosome 1 open reading frame 2	C1orf2

Hs.199695	1	205	694	**212282_at**	**212282_at**	7	2	0	0	0	0	201	947	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212282_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=199695	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=199695	Human MAC30 mRNA, 3' end /cds=(0,569) /gb=L19183 /gi=307154 /ug=Hs.199695 /len=2002	Hs.199695	hypothetical protein MAC30

Hs.201967	1	206	695	**211653_x_at**	**211653_x_at**	10	7	5	0	0	0	651	197	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211653_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=201967	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=201967	Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(0,971) /gb=NM_001354 /gi=4503284 /ug=Hs.201967 /len=972	Hs.201967	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	AKR1C2

Hs.20295	1	207	696	**205394_at**	**205394_at**	13	7	1	1	0	0	336	469	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205394_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20295	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20295	Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA /cds=(34,1464) /gb=NM_001274 /gi=4502802 /ug=Hs.20295 /len=1821	Hs.20295	CHK1 checkpoint homolog (S. pombe) CHEK1

Hs.21016

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208

697

205229_s_at

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205229_s_at 7 7 5 2 1 6 949 405 2

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http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=205229_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=21016

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=21016

/gb=NM_004086 /gi=4758021 /ug=Hs.21016 /len=2534 /cds=(56,1708)

Homo sapiens coagulation factor C homolog, cochlin (Limulus polyphemus) (COCH), mRNA

coagulation factor C homolog, cochlin (Limulus polyphemus)

COCH

Hs.21016

Hs.211556

1

209

698

204256_at

204256_at

10 7 6 2 0 0 0 641 267 2 1

1

&chip_id=2 1556 1556 56 /len=3045

d=204256_at =Hs&CID=21 =Hs&CID=21 /ug=Hs.2115

pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=13129087

obeset_anno. v/UniGene/cl v/UniGene/cl 090

eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_024

bin/elke/prob http://www.nc http://www.nc 77)

gi-

metagen.de/c

http://intranet.

/cds=(280,10

mRNA

(LCE),

MGC5487

protein

hypothetical

sapiens

Homo

long-chain fatty-acyl elongase

LCE

Hs.211556

ABCA1

ATP-binding cassette, sub-family A (ABC1), member 1

Hs.211562

1
210
699
203505_at
203505_at
203505_at
9 6 4 2 1 0 579 771 2 1

1

Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA /cds=(120,6725) /gi-4557805 /gb=NM_005502 /ug=Hs.211562 /len=9497

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info?probeset_id=2&chip_id=2 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=21 1562

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=21 1562

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=nucleotide&cmd=search&term=NM_005502 /gb=NM_005502 /gi=4557805 /ug=Hs.211562 /len=9497

Hs.22835

1
212
701
222803_at
222803_at
11 7 3 0 1 0 221 500 3

1 835 1

http://intranet.metagen.de/cgi-bin/eike/prob_eset_anno/pr_obeset_anno.pl?probeset_id=222803_at&chip_id=3

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22835

/gb=AK021950 /gi=10433254 /ug=Hs.22835 /len=1926

HHGP protein HHGP

Hs.21275

1
211
700
222657_s_at
222657_s_at
10 7 1 1 1 0 0 306 632 3

1 275 1

http://intranet.metagen.de/cgi-bin/eike/prob_eset_anno/pr_obeset_anno.pl?probeset_id=222657_s_at&chip_id=3

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=21275

/cds=(3,458) /gb=NM_018299 /gi=8922821 /ug=Hs.21275 /len=2201

Homo sapiens hypothetical protein FLJ11011 (FLJ11011), mRNA

hypothetical protein FLJ11011 FLJ11011

Homo sapiens cDNA FLJ11888 fis, clone HEMBA1007243, weakly similar to Chinese hamster hprt mRNA /cds=(29,706

Hs.236494	1	213	702	222981_s_at	222981_s_at	13	11	7	0	0	0	36	195	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222981_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=236494	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=236494	Homo sapiens RAB10, member RAS oncogene family (RAB10), mRNA /cds=(90,692) /gb=NM_016131 /gi=7705848 /ug=Hs.236494 /len=3164	Hs.236494	RAB10, member RAS oncogene family	RAB10

Hs.23900	1	214	703	**222077_s_at**	**222077_s_at**	12	12	9	1	1	0	387	132	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222077_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23900	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23900	Homo sapiens Rac GTPase activating protein 1 (RACGAP1), mRNA /cds=(70,1968) /gb=NM_013277 /gi=7019432 /ug=Hs.23900 /len=3050	Hs.23900	Rac GTPase activating protein 1	RACGAP1

Hs.239527	1	215	704	**227897_at**	**227897_at**	13	10	9	4	0	0	431	110	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=227897_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239527	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239527	Homo sapiens, clone MGC:20484 IMAGE:4650072, mRNA, complete cds /cds=(424,975) /gb=BC012362 /gi=15214477 /ug=Hs.239527 /len=1913	Hs.239527	RAP2B, member of RAS oncogene family	RAP2B
Hs.23960	1	216	705	**214710_s_at**	**214710_s_at**	12	12	10	2	0	0	105	156	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=214710_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23960	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23960	Homo sapiens cyclin B1 (CCNB1), mRNA /cds=(177,1478) /gb=NM_031966 /gi=14327895 /ug=Hs.23960 /len=1578	Hs.23960	cyclin B1	CCNB1

Hs.239727	1	217	706	**204751_x_at**	**204751_x_at**	12	12	10	3	1	0	539	194	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204751_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239727	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239727	Homo sapiens desmocollin 2 (DSC2), transcript variant Dsc2b, mRNA /cds=(201,2744) /gb=NM_004949 /gi=13435365 /ug=Hs.239727 /len=3500	Hs.239727	desmocollin 2	DSC2

Hs.2442	1	218	707	**202381_at**	**202381_at**	7	5	5	1	1	0	887	674	2	1	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202381_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2442	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2442	Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA /cds=(78,2537) /gb=NM_003816 /gi=4501914 /ug=Hs.2442 /len=3865	Hs.2442	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	ADAM9

Hs.250773	1	219	708	**200891_s_at**	**200891_s_at**	6	3	0	0	0	0	370	1247	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200891_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=250773	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=250773	Homo sapiens signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(111,971) /gb=NM_003144 /gi=6552340 /ug=Hs.250773 /len=3285	Hs.250773	signal sequence receptor, alpha (translocon-associated protein alpha)	SSR1

Hs.250822

1

220

709

204092_s_at

204092_s_at

204092_s_at

13 12 12 2 0 0 31 82 2 1 1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204092_s_at&chip_id=20822 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=250822 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=250822 http://www.ncbi.nlm.nih.gov/gb=NM_003600 /gi=4507274 /ug=Hs.250822 /len=2253

Homo sapiens serine/threonine kinase 15 (STK15), mRNA /cds=(256,1467)

serine/threonine kinase 15

STK15

Hs.25740	1	221	710	222646_s_at	222646_s_at	12	8	7	6	1	0	746	140	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222646_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25740	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25740	Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), mRNA /cds=(226,1632) /gb=NM_014584 /gi=7657068 /ug=Hs.25740 /len=3334	Hs.25740	ERO1-like (S. cerevisiae) ERO1L

Hs.260622	1	222	711	**217777_s_at**	**217777_s_at**	7	2	0	0	0	6	73	1031	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217777_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=260622	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=260622	Homo sapiens cDNA FLJ14515 fis, clone NT2RM1000800, weakly similar to Mus musculus partial mRNA for B-IND1 protein /cds=(115,1203) /gb=AK027421 /gi=14042085 /ug=Hs.260622 /len=3170	Hs.260622	butyrate-induced transcript 1 HSPC121

Hs.263727	1	223	712	**222654_at**	**222654_at**	12	8	5	0	0	0	348	286	3	1	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222654_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=263727	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=263727	Homo sapiens hypothetical protein FLJ20421 (FLJ20421), mRNA /cds=(283,1362) /gb=NM_017813 /gi=8923391 /ug=Hs.263727 /len=1668	Hs.263727	uk1

CBX3

chromobox homolog 3 (HP1 gamma homolog, Drosophila)

Hs.278554

Hs.278554	1	224	713	**200037_s_at**	**200037_s_at**	8	1	0	0	0	0	238	1217	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200037_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=278554	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=278554	Homo sapiens chromobox homolog 3 (HP1 gamma homolog, Drosophila) (CBX3), mRNA /cds=(111,662) /gb=NM_007276 /gi=15082257 /ug=Hs.278554 /len=1833

Hs.279610	1	225	714	**218772_x_at**	**218772_x_at**	11	7	5	0	0	0	281	472	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218772_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279610	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279610	Homo sapiens hypothetical protein FLJ10493 (FLJ10493), mRNA /cds=(117,992) /gb=NM_018112 /gi=8922460 /ug=Hs.279610 /len=2076	Hs.279610	hypothetical protein FLJ10493	FLJ10493
Hs.279916	1	226	715	**214164_x_at**	**214164_x_at**	8	5	4	3	2	3	1125	829	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=214164_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279916	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279916	Homo sapiens hypothetical protein FLJ20151 (FLJ20151), mRNA /cds=(2,427) /gb=NM_017689 /gi=8923149 /ug=Hs.279916 /len=2051	Hs.279916	hypothetical protein FLJ20151	FLJ20151

Hs.283558	1	227	716	**234464_s_at**	**234464_s_at**	11	7	2	0	0	0	149	516	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=234464_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283558	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283558	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA /cds=(35,517) /gb=NM_018509 /gi=8924089 /ug=Hs.283558 /len=2341	Hs.283558	hypothetical protein PRO1855	PRO1855
Hs.283713	1	228	717	**225681_at**	**225681_at**	13	12	12	7	1	0	685	28	3		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225681_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283713	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283713	Homo sapiens, Similar to RIKEN cDNA 1110014B07 gene, clone MGC:20766 IMAGE:4586039, mRNA, complete cds /cds=(108,839) /gb=BC014245 /gi=15559789 /ug=Hs.283713 /len=1245	Hs.283713	hypothetical protein BC014245	LOC115908

Hs.2841	1	229	718	**206023_at**	**206023_at**	6	5	5	4	1	7	773	89	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206023_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2841	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2841	Homo sapiens neuromedin U (NMU), mRNA /cds=(105,629) /gb=NM_006681 /gi=5729946 /ug=Hs.2841 /len=817	Hs.2841	neuromedin U NMU

Hs.288757

1

230

719

214435_x_at

214435_x_at

214435_x_at

11 10 4 3 0 0 287 263 2 1 1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=2&at&chip_id=2&d=214435_x_at 8757

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28 8757

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28 8757

/cds=(0,629) /gb=NM_005402 /gi=4885568 /ug=Hs.2887 57 /len=630

Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA

Hs.288757

v-ral simian leukemia viral oncogene homolog A (ras related)

RALA

Hs.300697	1	231	720	•211430_s_at	211430_s_at	6	6	6	4	4	1	1093	521	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211430_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=300697	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=300697	Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m marker), clone MGC:20691 IMAGE:4766140, mRNA, complete cds /cds=(72,1706) /gb=BC019046 /gi=17512135 /ug=Hs.300697 /len=3143	Hs.300697	immunoglobulin heavy constant gamma 3 (G3m marker) IGHG3

Hs.30524	1	232	721	204668_at	204668_at	7	1	0	0	0	3	197	1020	2	1		1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204668_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30524	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30524	Homo sapiens ring finger protein 24 (RNF24), mRNA /cds=(252,698) /gb=NM_007219 /gi=10518498 /ug=Hs.30524 /len=1692	Hs.30524	ring finger protein 24 RNF24
Hs.3104	1	233	722	206364_at	206364_at	10	10	5	1	1	2	570	268	2		1		1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206364_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=3104	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=3104	Homo sapiens KIAA0042 gene product (KIAA0042), mRNA /cds=(439,5385) /gb=NM_014875 /gi=7661877 /ug=Hs.3104 /len=6586	Hs.3104	KIAA0042 gene product KIAA0042

Hs.311	1	234	723	209434_s_at	209434_s_at	11	4	0	0	0	0	237	771	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209434_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=311	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=311	Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds /cds=(50,1603) /gb=U00238 /gi=404860 /ug=Hs.311 /len=3608	Hs.311	phosphoribosyl pyrophosphate amidotransferase PPAT

Hs.314452	1	235	724	**224279_s_at**	**224279_s_at**	10	9	6	2	0	2	700	163	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224279_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=314452	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=314452	Homo sapiens fibrousheathin II (FSP-2), mRNA /cds=(48,1529) /gb=NM_012189 /gi=6912377 /ug=Hs.314452 /len=2228

Hs.314452	calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	CABYR

Hs.31664	1	236	725	**219764_at**	**219764_at**	11	7	3	0	1	2	662	319	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219764_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31664	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31664	Homo sapiens frizzled homolog 10 (Drosophila) (FZD10), mRNA /cds=(17,1762) /gb=NM_007197 /gi=6005761 /ug=Hs.31664 /len=2811	Hs.31664	frizzled homolog 10 (Drosophila)	FZD10

Hs.323114	1	237	726	**219402_s_at**	**219402_s_at**	11	7	2	0	0	0	83	571	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219402_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323114	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323114	Homo sapiens cDNA FLJ13784 fis, clone PLACE4000593 /cds=UNKNOWN /gb=AK023846 /gi=10435906 /ug=Hs.323114 /len=5524	Hs.323114	hypothetical protein MGC3067 MGC3067
Hs.324275	1	238	727	**212637_s_at**	**212637_s_at**	7	5	4	1	0	0	652	937	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212637_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=324275	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=324275	Homo sapiens WW domain-containing protein 1 (WWP1), mRNA /cds=(10,2778) /gb=NM_007013 /gi=13654238 /ug=Hs.324275 /len=3382	Hs.324275	WW domain-containing protein 1 WWP1

Hs.333116	1	239	728	208079_s_at	208079_s_at	13	13	13	7	0	0	12	55	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208079_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=333116	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=333116	Homo sapiens serine/threonine kinase 6 (STK6), mRNA /cds=(169,1377) /gb=NM_003158 /gi=4507278 /ug=Hs.333116 /len=2033	Hs.333116
Hs.334562	1	240	729	203213_at	203213_at	11	9	5	1	0	0	320	257	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203213_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334562	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334562	Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 1, mRNA /cds=(129,1022) /gb=NM_001786 /gi=16306490 /ug=Hs.334562 /len=1235	Hs.334562

Hs.3446	1	241	730	**202670_at**	**202670_at**	8	7	4	1	1	0	644	657	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202670_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=3446	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=3446	Homo sapiens mitogen-activated protein kinase kinase 1 (MAP2K1), mRNA /cds=(72,1253) /gb=NM_002755 /gi=14589898 /ug=Hs.3446 /len=2222	Hs.3446	mitogen-activated protein kinase kinase 1 MAP2K1

Hs.348669	1	242	731	**201897_s_at**	**201897_s_at**	12	10	9	2	0	0	382	221	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201897_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348669	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348669	Homo sapiens CDC28 protein kinase 1 (CKS1), mRNA /cds=(9,248) /gb=NM_001826 /gi=4502856 /ug=Hs.348669 /len=717	Hs.348669
Hs.348994	1	243	732	**202007_at**	**202007_at**	8	5	5	1	1	5	713	740	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202007_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348994	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348994	Homo sapiens nidogen (enactin) (NID), mRNA /cds=(90,3833) /gb=NM_002508 /gi=4505394 /ug=Hs.348994 /len=4898	Hs.348994

Hs.349506	1	244	733	**224586_x_at**	**224586_x_at**	11	6	0	0	0	0	212	513	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224586_x_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349506	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=349506	Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(0,383) /gb=NM_006713 /gi=5729967 /ug=Hs.349506 /len=384	Hs.349506

Hs.35542

1
246
735
218930_s_at
218930_s_at
10 7 5 0 1 0 556 461 2 1

1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/obeset_anno.pl?probeset_id=218930_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=35

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=35

42

42

hypothetical protein FLJ11273 (FLJ11273), mRNA /cds=(130,954)

/gb=NM_018374

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/ug=Hs.35422

/len=2067

FLJ11273

TM4SF1

Hs.351316

1
245
734
209387_s_at
209387_s_at
12 11 10 5 1 0 710 64 2 1

1 1

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http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=35

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=35

1316

1316

Homo sapiens, Similar to transmembrane 4 superfamily member 1, clone MGC:14656 IMAGE:4101110, mRNA, complete cds /cds=(101,709)

/gb=BC008442

/gi=14250074

/ug=Hs.351316

/len=1584

Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA /cds=(130,954)

/gb=NM_018374

/gi=8922965

/ug=Hs.35422

/len=2067

Hs.36708	1	247	736	**203755_at**	**203755_at**	13	10	3	0	0	0	188	334	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203755_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=36708	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=36708	Homo sapiens BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast) (BUB1B), mRNA /cds=(42,3194) /gb=NM_001211 /gi=5729749 /ug=Hs.36708 /len=3583	Hs.36708	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast) BUB1B

Hs.394	1	248	737	**202912_at**	**202912_at**	11	8	5	2	1	0	596	155	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202912_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=394	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=394	Homo sapiens adrenomedullin (ADM), mRNA /cds=(156,713) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	Hs.394	adrenomedullin	ADM

Hs.4295	1	249	738	**202352_s_at**	**202352_s_at**	12	6	1	0	0	0	141	549	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202352_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=4295	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=4295	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA /cds=(43,1413) /gb=NM_002816 /gi=4506220 /ug=Hs.4295 /len=3548	Hs.4295	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 PSMD12
Hs.5199	1	250	739	**223229_at**	**223229_at**	11	9	6	0	0	2	94	232	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223229_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5199	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5199	Homo sapiens HSPC150 protein similar to ubiquitin-conjugating enzyme (HSPC150), mRNA /cds=(126,719) /gb=NM_014176 /gi=7661807 /ug=Hs.5199 /len=928	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzyme HSPC150

Hs.54649	1	251	740	**212438_at**	**212438_at**	9	5	1	0	0	2	243	678	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212438_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=54649	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=54649	Homo sapiens, clone MGC:22775 IMAGE:4699198, mRNA, complete cds /cds=(27,494) /gb=BC017890 /gi=17389747 /ug=Hs.54649 /len=1433	Hs.54649	putative nucleic acid binding protein RY-1	RY1

Hs.61635	1	252	741	**205542_at**	**205542_at**	9	6	4	1	1	1	774	389	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205542_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=61635	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=61635	Homo sapiens six transmembrane epithelial antigen of the prostate (STEAP), mRNA /cds=(65,1084) /gb=NM_012449 /gi=9558758 /ug=Hs.61635 /len=1195	Hs.61635	six transmembrane epithelial antigen of the prostate	STEAP

Hs.62275	1	253	742	218193_s_at	218193_s_at	10	7	7	0	1	0	642	462	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218193_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=62275	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=62275	Homo sapiens mRNA; cDNA DKFZp761G2423 (from clone DKFZp761G2423); complete cds /cds=(58,474) /gb=AL136571 /gi=7018429 /ug=Hs.62275 /len=2946	Hs.62275	CGI-141 protein	LOC51026

Hs.656	1	254	743	**205167_s_at**	**205167_s_at**	8	2	0	0	0	5	103	823	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205167_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=656	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=656	Homo sapiens cell division cycle 25C (CDC25C), transcript variant 1, mRNA /cds=(270,1691) /gb=NM_001790 /gi=12408659 /ug=Hs.656 /len=2115	Hs.656	cell division cycle 25C	CDC25C

Hs.6682

1

255

744

209921_at

209921_at

209921_at

9 8 6 3 2 2 2 1

837

222

1

Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA /cds=(0,1505) /gb=NM_014331 /gi=18141306 /ug=Hs.6682 /len=3144

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=2&chip_id=2 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORGANISM=Hs&CID=66822 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORGANISM=Hs&CID=66822 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORGANISM=Hs&CID=66822

Hs.6682

solute carrier family 7, (cationic amino acid transporter, y+ system) member 11

SLC7A11

Hs.69328

1

256

745

206584_at

206584_at

7 5 4 1 0 0 710 890 2

1 1

&chip_id=2 328 328 8 /len=624

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bin/eike/prob http://www.nc http://www.nc 7)

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http://intranet.

Homo sapiens MD-2 protein (MD-2), mRNA /cds=(125,60

Hs.69328

MD-2 protein

MD-2

Hs.74471

1

257

746

201667_at

201667_at

201667_at

13 12 12 9 1 0 343 9 2 1

1

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http://intranet.

/cds=(207,13

mRNA

(GJA1),

(connexin 43)

1, 43kD

protein, alpha

junction

sapiens gap

Homo

gap junction protein, alpha 1, 43kD (connexin 43)

GJA1

Hs.74471

Hs.75360

1

258

747

201117_s_at

201117_s_at

201117_s_at

9 6 5 0 2 0 893 723 2

1 1

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obeset_anno. v/UniGene/cl v/UniGene/cl 873

eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_001

bin/eike/prob http://www.nc http://www.nc 20)

gi- /cds=(290,17

metagen.de/c mRNA

http://intranet. (CPE),

dase E

carboxypepti

sapiens

Homo

carboxypeptidase E

CPE

Hs.75360

Hs.75393	1	259	748	**215227_x_at**	**215227_x_at**	13	12	11	2	0	0	174	148	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215227_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75393	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75393	Homo sapiens acid phosphatase 1, soluble (ACP1), transcript variant a, mRNA /cds=(775,1251) /gb=NM_004300 /gi=4757713 /ug=Hs.75393 /len=2222	Hs.75393	acid phosphatase 1, soluble ACP1

Hs.75498

1
260
749
205476_at
205476_at
205476_at
5 4 4 3 3 6
1185
2045
2 1 1

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Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA /cds=(58,348 http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75591 /gb=NM_004591 /gi=4759075 /ug=Hs.75498

Hs.75498
small inducible cytokine subfamily A (Cys-Cys), member 20
SCYA20

Hs.75617

1

261

750

211964_at

211964_at

211964_at

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1

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bin/eike/prob http://www.nc http://www.nc 26)

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http://intranet.

Homo
sapiens
collagen,
type IV, alpha
2 (COL4A2),
mRNA
/cds=(288,54

Hs.75617

collagen, type IV, alpha 2
COL4A2

Hs.75875	1	262	751	**201001_s_at**	**201001_s_at**	12	8	4	0	0	0	51	301	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201001_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75875	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75875	Homo sapiens mRNA; cDNA DKFZp564H192 (from clone DKFZp564H192) /cds=UNKNOWN /gb=AL110132 /gi=5817027 /ug=Hs.75875 /len=4189	Hs.75875	ubiquitin-conjugating enzyme E2 variant 1	UBE2V1

Hs.75981	1	263	752	**201672_s_at**	**201672_s_at**	12	4	1	0	0	0	351	652	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201672_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75981	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75981	Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), mRNA /cds=(91,1575) /gb=NM_005151 /gi=4827049 /ug=Hs.75981 /len=2481	Hs.75981	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	USP14

Hs.76691	1	264	753	**218032_at**	**218032_at**	6	3	3	0	0	0	302	1007	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218032_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76691	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76691	Homo sapiens stannin mRNA, complete cds /cds=(175,441) /gb=AF070673 /gi=3978241 /ug=Hs.76691 /len=3295	Hs.76691	stannin SNN

Hs.76941	1	265	754	**208836_at**	**208836_at**	13	9	9	2	1	0	284	150	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208836_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76941	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76941	Homo sapiens ATPase, Na+/K+ transporting, beta 3 polypeptide (ATP1B3), mRNA /cds=(0,839) /gb=NM_001679 /gi=4502280 /ug=Hs.76941 /len=1679	Hs.76941	ATPase, Na+/K+ transporting, beta 3 polypeptide ATP1B3

Hs.77152	1	266	755	**208795_s_at**	**208795_s_at**	11	6	2	0	0	0	125	690	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208795_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77152	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77152	Homo sapiens MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) (MCM7), mRNA /cds=(544,2175) /gb=NM_005916 /gi=14149622 /ug=Hs.77152 /len=2327	Hs.77152	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	MCM7

Hs.77171	1	267	756	**216237_s_at**	**216237_s_at**	10	5	1	0	0	0	46	668	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=216237_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77171	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77171	Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (MCM5), mRNA /cds=(82,2283) /gb=NM_006739 /gi=6981191 /ug=Hs.77171 /len=2525	Hs.77171	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	MCM5

Hs.77274	1	268	757	**205479_s_at**	**205479_s_at**	11	8	7	3	1	1	788	157	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205479_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77274	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77274	Homo sapiens plasminogen activator, urokinase (PLAU), mRNA /cds=(76,1371) /gb=NM_002658 /gi=4505862 /ug=Hs.77274 /len=2304	Hs.77274	plasminogen activator, urokinase	PLAU

Hs.77326	1	269	758	**210095_s_at**	**210095_s_at**	6	6	5	2	0	0	953	899	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210095_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77326	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77326	Human insulin-like growth factor-binding protein-3 gene, complete cds, clone HL1006d /cds=(132,1007) /gb=M35878 /gi=184522 /ug=Hs.77326 /len=3446	Hs.77326	insulin-like growth factor binding protein 3	IGFBP3

Hs.77367	1	270	759	**203915_at**	**203915_at**	9	4	4	3	2	1	815	1202	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203915_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77367	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77367	Homo sapiens monokine induced by gamma interferon (MIG), mRNA /cds=(39,416) /gb=NM_002416 /gi=4505186 /ug=Hs.77367 /len=2545	Hs.77367	monokine induced by gamma interferon MIG

GCSH

glycine cleavage system protein H (aminomethyl carrier)

Hs.77631

Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH), mRNA /cds=(24,545 /gi-

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213129_s_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77631

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77631

http://www.ncbi.nlm.nih.gov/gb=NM_004483 /gi=4758423 /ug=Hs.7763 1 /len=1086

631

1 1

2

542

471

0 0

1 0

3 1

8 3

9 8

213129_s_at

213129_s_at

213129_s_at

760

271

1

Hs.77631

Hs.77719	1	272	761	**214005_at**	**214005_at**	11	9	4	0	0	0	145	344	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=214005_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77719	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=77719	Homo sapiens gamma-glutamyl carboxylase (GGCX), mRNA /cds=(86,2362) /gb=NM_000821 /gi=4503984 /ug=Hs.77719 /len=2460	Hs.77719	gamma-glutamyl carboxylase GGCX

Hs.78619	1	273	762	**203560_at**	**203560_at**	11	9	8	2	1	0	276	121	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203560_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78619	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78619	Homo sapiens gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) (GGH), mRNA /cds=(59,1015) /gb=NM_003878 /gi=4503986 /ug=Hs.78619 /len=1280	Hs.78619	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	GGH

Hs.78771	1	274	763	**200737_at**	**200737_at**	12	7	6	1	1	0	499	241	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200737_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78771	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78771	Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA /cds=(79,1332) /gb=NM_000291 /gi=4505762 /ug=Hs.78771 /len=1767	Hs.78771	phosphoglycerate kinase 1 PGK1

Hs.79284

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http://www.nc
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v/UniGene/cl
ust.cgi?ORG
=Hs&CID=79
284

http://www.nc
bi.nlm.nih.go
v/UniGene/cl
ust.cgi?ORG
=Hs&CID=79
284

Homo
sapiens
mesoderm
specific
transcript
homolog
(mouse)
(MEST),
mRNA
/cds=(223,12
30)
/gb=NM_002
402
/gi=4505154
/ug=Hs.7928
4 /len=2476

Hs.79284

mesoderm specific transcript homolog
(mouse)
MEST

monocyte to macrophage differentiation-associated
MMD

Hs.79889

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276
765
203414_at
203414_at
10 8 4 1 1 1 632 574 2 1
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Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA /cds=(81,797 /gb=NM_012329 /gi=6912507 /ug=Hs.79889 /len=2533

Hs.79914	1	277	766	**201744_s_at**	**201744_s_at**	7	7	5	1	2	0	1007	412	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201744_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79914	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79914	Homo sapiens lumican (LUM), mRNA /cds=(84,1100) /gb=NM_002345 /gi=4505046 /ug=Hs.79914 /len=1717	Hs.79914	lumican	LUM

Hs.80612	1	278	767	**201898_s_at**	**201898_s_at**	11	6	5	0	1	0	449	571	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201898_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80612	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80612	Homo sapiens ubiquitin-conjugating enzyme E2A (RAD6 homolog) (UBE2A), mRNA /cds=(120,578) /gb=NM_003336 /gi=4507768 /ug=Hs.80612 /len=1743	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A

Hs.80962	1	279	768	**206291_at**	**206291_at**	6	6	6	5	2	5	796	277	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206291_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80962	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80962	Homo sapiens neurotensin (NTS), mRNA /cds=(110,622) /gb=NM_006183 /gi=6006028 /ug=Hs.80962 /len=838	Hs.80962	neurotensin NTS

Hs.80976	1	280	769	212023_s_at	212023_s_at	6	2	2	0	0	8	206	706	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212023_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80976	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80976	H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67 /cds=(196,9966) /gb=X65550 /gi=415818 /ug=Hs.80976 /len=12515	Hs.80976	antigen identified by monoclonal antibody Ki-67 MKI67

Hs.82226	1	281	770	**201141_at**	**201141_at**	13	12	12	8	0	0	49	8	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201141_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82226	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82226	Homo sapiens glycoprotein (transmembrane) nmb (GPNMB), mRNA /cds=(91,1773) /gb=NM_002510 /gi=4505404 /ug=Hs.82226 /len=2669	Hs.82226	glycoprotein (transmembrane) nmb GPNMB

Hs.82314	1	282	771	**202854_at**	**202854_at**	13	11	7	1	1	0	277	224	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202854_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82314	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82314	Homo sapiens hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) (HPRT1), mRNA /cds=(85,741) /gb=NM_000194 /gi=4504482 /ug=Hs.82314 /len=1331	Hs.82314	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	HPRT1

Hs.83169	1	283	772	**204475_at**	**204475_at**	10	8	7	6	2	0	980	78	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204475_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83169	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83169	Homo sapiens matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA /cds=(71,1480) /gb=NM_002421 /gi=13027798 /ug=Hs.83169 /len=1973	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	MMP1

Hs.83758	1	284	773	**204170_s_at**	**204170_s_at**	13	12	12	7	0	0	63	36	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204170_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83758	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83758	Homo sapiens CDC28 protein kinase 2 (CKS2), mRNA /cds=(95,334) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627	Hs.83758	CDC28 protein kinase 2	CKS2
Hs.83883	1	285	774	**222449_at**	**222449_at**	9	5	4	1	2	0	738	944	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222449_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83883	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83883	Homo sapiens STAG1/PMEPA1 mRNA, complete cds /cds=(320,1183) /gb=AF305616 /gi=16303741 /ug=Hs.83883 /len=4839	Hs.83883	transmembrane, prostate androgen induced RNA	TMEPAI

Hs.89545

1

286

775

202243_s_at

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10 7 5 1 1 1 0 591 663 2 1 1

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http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=89545

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545 545

Homo sapiens proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(23,817 /gb=NM_002796 /gi=4506198 /ug=Hs.89545 5 /len=925

Hs.89545

proteasome (prosome, macropain) subunit, beta type, 4

PSMB4

Hs.9700	1	287	776	**213523_at**	**213523_at**	5	3	1	0	0	5	334	898	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213523_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9700	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9700	Homo sapiens cyclin E1 (CCNE1), transcript variant 1, mRNA /cds=(183,1415) /gb=NM_001238 /gi=17318558 /ug=Hs.9700 /len=1958	Hs.9700	cyclin E1 CCNE1

Hs.98074	1	288	777	**209744_x_at**	**209744_x_at**	9	7	3	0	1	3	509	442	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209744_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=98074	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=98074	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA /cds=(6,2594) /gb=NM_031483 /gi=14010858 /ug=Hs.98074 /len=2970	Hs.98074	itchy homolog E3 ubiquitin protein ligase (mouse)	ITCH
	1	289	778	**212460_at**	**212460_at**	11	7	6	1	1	0	555	213	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212460_at&chip_id=2						uk5

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290																			
779																			
201114_x_at																			
201114_x_at																			
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11	4	3	0	0	1	69	434	2		1									1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201114_x_at&chip_id=2

Hs.100431	2	291	780	205242_at2	**205242_at**	4	4	4	2	1	7	751	1222	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205242_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=100431	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=100431	Homo sapiens small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-cell chemoattractant) (SCYB13), mRNA /cds=(90,419) /gb=NM_006419 /gi=5453576 /ug=Hs.100431 /len=1216	Hs.100431	small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-cell chemoattractant)	SCYB13

Hs.1012	2	292	781	205654_at2	**205654_at**	5	4	0	0	4	0	1075	1760	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205654_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1012	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1012	Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA /cds=(138,1931) /gb=NM_000715 /gi=4502502 /ug=Hs.1012 /len=2178	Hs.1012	complement component 4 binding protein, alpha C4BPA

Hs.102122	2	293	782	205302_at2	**205302_at**	3	3	3	3	0	9	591	1248	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205302_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=102122	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=102122	Homo sapiens insulin-like growth factor binding protein 1 (IGFBP1), mRNA /cds=(165,944) /gb=NM_000596 /gi=4504614 /ug=Hs.102122 /len=1514	Hs.102122	insulin-like growth factor binding protein 1	IGFBP1

Hs.103834	2	294	783	201764_at2	**201764_at**	4	1	1	0	0	8	113	529	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201764_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103834	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103834	Homo sapiens hypothetical protein MGC5576 (MGC5576), mRNA /cds=(51,803) /gb=NM_024056 /gi=13129025 /ug=Hs.103834 /len=1472	Hs.103834	hypothetical protein MGC5576 MGC5576

Hs.103982	2	295	784	210163_at2	**210163_at**	7	5	5	2	0	3	732	394	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210163_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103982	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=103982	Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 11 (SCYB11), mRNA /cds=(93,377) /gb=NM_005409 /gi=14790145 /ug=Hs.103982 /len=1493	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), member 11	SCYB11

Hs.104433	2	296	785	228055_at3	**228055_at**	4 4 3 0 0 8	200	140	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=228055_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104433	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=104433	Homo sapiens napsin 2 precursor, mRNA, partial sequence /cds=UNKNOWN /gb=AF098485 /gi=4235426 /ug=Hs.104433 /len=1353	Hs.104433 Homo sapiens napsin 2 precursor, mRNA, partial sequence
Hs.105460	2	297	786	204687_at2	**204687_at**	7 5 2 1 0 1	557	396	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204687_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=105460	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=105460	Homo sapiens DKFZP564O0823 protein (DKFZP564O0823), mRNA /cds=(170,904) /gb=NM_015393 /gi=7661631 /ug=Hs.105460 /len=2155	Hs.105460 DKFZP564O0823 protein DKFZP564O0823

Hs.106260	2	298	787	218404_at2	**218404_at**	9	6	6	1	0	1	116	158	2	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218404_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106260	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106260	Homo sapiens sorting nexin 10 (SNX10), mRNA /cds=(128,733) /gb=NM_013322 /gi=7019536 /ug=Hs.106260 /len=2480	Hs.106260	sorting nexin 10	SNX10
Hs.106825	2	299	788	219732_at2	**219732_at**	4	3	2	1	1	0	907	219	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219732_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106825	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=106825	Homo sapiens hypothetical protein FLJ20300 (FLJ20300), mRNA /cds=(266,1243) /gb=NM_017753 /gi=8923280 /ug=Hs.106825 /len=2331	Hs.106825	hypothetical protein FLJ20300	FLJ20300

Hs.107	2	300	789	205305_at2	**205305_at**	9	9	9	7	0	2	193	4	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205305_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=107	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=107	Homo sapiens fibrinogen-like 1 (FGL1), mRNA /cds=(78,1016) /gb=NM_004467 /gi=4758371 /ug=Hs.107 /len=1215	Hs.107	fibrinogen-like 1 FGL1

Hs.109225	2	301	790	203868_s_at2	**203868_s_at**	7	7	5	1	1	0	362	84	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203868_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=109225	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=109225	Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA /cds=(120,2339) /gb=NM_001078 /gi=18201907 /ug=Hs.109225 /len=3119	Hs.109225	vascular cell adhesion molecule 1	VCAM1

Hs.1104	2	302	791	205430_at2	**205430_at**	4	4	4	1	0	5	765	926	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205430_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1104	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1104	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA /cds=(698,2062) /gb=NM_021073 /gi=10835090 /ug=Hs.1104 /len=2153	Hs.1104	bone morphogenetic protein 5	BMP5
Hs.112208	2	303	792	220057_at2	**220057_at**	5	5	5	2	0	7	548	185	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=220057_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112208	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112208	Homo sapiens XAGE-1 protein (XAGE-1), mRNA /cds=(85,525) /gb=NM_020411 /gi=9966898 /ug=Hs.112208 /len=626	Hs.112208	G antigen, family D, 2	GAGED2

Hs.112242	2	304	793	223484_at3	**223484_at**	7	5	4	0	2	0	544	274	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223484_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112242	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=112242	Homo sapiens normal mucosa of esophagus specific 1 (NMES1), mRNA /cds=(189,440) /gb=NM_032413 /gi=14165279 /ug=Hs.112242 /len=886	Hs.112242	normal mucosa of esophagus specific 1	NMES1
Hs.114948	2	305	794	206315_at2	**206315_at**	6	4	1	1	1	2	524	919	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206315_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=114948	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=114948	Homo sapiens cytokine receptor-like factor 1 (CRLF1), mRNA /cds=(118,1386) /gb=NM_004750 /gi=4758061 /ug=Hs.114948 /len=1716	Hs.114948	cytokine receptor-like factor 1	CRLF1

Hs.11565	2	306	795	224972_at3	**224972_at**	3	2	0	0	1	4	816	436	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224972_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11565	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=11565	Homo sapiens chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(163,402) /gb=NM_080748 /gi=18152784 /ug=Hs.11565 /len=602	Hs.11565

chromosome 20 open reading frame 52

C20orf52

Hs.115770	2	307	796	210643_at2	**210643_at**	5	4	3	1	0	6	554	939	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210643_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115770	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115770	Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 1, mRNA /cds=(156,1109) /gb=NM_003701 /gi=14790148 /ug=Hs.115770 /len=2226	Hs.115770	tumor necrosis factor (ligand) superfamily, member 11	TNFSF11

Hs.115907	2	308	797	208072_s_at2	**208072_s_at**	7	2	1	0	0	1	505	302	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208072_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115907	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115907	Homo sapiens diacylglycerol kinase, delta (130kD) (DGKD), mRNA /cds=(80,3589) /gb=NM_003648 /gi=4503310 /ug=Hs.115907 /len=6207	Hs.115907	diacylglycerol kinase, delta (130kD)	DGKD

Hs.115912	2	309	798	223779_at3	**223779_at**	9	7	7	4	0	2	153	40	3		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223779_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115912	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=115912	Homo sapiens hypothetical protein MGC10981 (MGC10981), mRNA /cds=(193,360) /gb=NM_032654 /gi=14249203 /ug=Hs.115912 /len=1685	Hs.115912	hypothetical protein MGC10981 MGC10981
Hs.119878	2	310	799	238025_at3	**238025_at**	4	0	0	0	0	1	308	746	3	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=238025_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=119878	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=119878	AL579387 Homo sapiens cDNA /clone=CS0DH004YA13 /gb=AL579387 /gi=12944382 /ug=Hs.119878 /len=784	Hs.119878	[illegible] gene, clone MGC:40065 IMAGE:5214733, mRNA, complete cds

Hs.121520	2	311	800	222108_at2	**222108_at**	5	2	1	1	2	0	549	419	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222108_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=121520	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=121520	Human BAC clone GS1-99H8 /cds=(0,1568) /gb=AC004010 /gi=2781385 /ug=Hs.121520 /len=1569	Hs.121520	Homo sapiens, clone IMAGE:3625286, mRNA, partial cds
Hs.13011	2	312	801	221050_s_at2	**221050_s_at**	2	1	1	1	0	10	47	90	2		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=221050_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13011	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=13011	Homo sapiens GTPBP2 mRNA for GTP-binding like protein 2, complete cds /cds=(191,1735) /gb=AB024574 /gi=9971157 /ug=Hs.13011 /len=2853	Hs.13011	GTP binding protein 2 GTPBP2

Hs.130181	2	313	802	217788_s_at2	**217788_s_at**	6	2	2	1	0	0	212	216	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217788_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=130181	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=130181	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), mRNA /cds=(0,1715) /gb=NM_004481 /gi=9945385 /ug=Hs.130181 /len=4447	Hs.130181	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	GALNT2

Hs.132781	2	314	803	222062_at2	**222062_at**	6	5	4	0	0	5	469	391	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222062_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=132781	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=132781	Homo sapiens class I cytokine receptor (WSX1), mRNA /cds=(423,2333) /gb=NM_004843 /gi=18379338 /ug=Hs.132781 /len=3258	Hs.132781	class I cytokine receptor	WSX1

Hs.132898	2	315	804	208964_s_at2	**208964_s_at**	6	1	1	0	0	1	322	505	2	1			1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208964_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=132898	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=132898	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA /cds=(80,1414) /gb=NM_013402 /gi=14141179 /ug=Hs.132898 /len=4213	Hs.132898	fatty acid desaturase 1	FADS1
Hs.1355	2	316	805	205927_s_at2	**205927_s_at**	4	4	3	1	4	0	932	1358	2		1	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205927_s_at&chip_id=255	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1355	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1355	Homo sapiens cathepsin E (CTSE), mRNA /cds=(49,1239) /gb=NM_001910 /gi=4503144 /ug=Hs.1355 /len=2158	Hs.1355	cathepsin E	CTSE

Hs.14570	2	317	806	212539_at2	**212539_at**	6	2	0	0	0	0	82	377	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212539_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=14570	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=14570	Homo sapiens, clone IMAGE:3355762, mRNA, partial cds /cds=UNKNOWN /gb=BC001171 /gi=12654664 /ug=Hs.14570 /len=2970	Hs.14570	hypothetical protein FLJ22530	FLJ22530

Hs.146360	2	318	807	201601_x_at2	**201601_x_at**	5	4	2	1	0	0	543	533	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201601_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=146360	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=146360	Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA /cds=(110,487) /gb=NM_003641 /gi=4504580 /ug=Hs.146360 /len=647	Hs.146360

interferon induced transmembrane protein 1 (9-27)

IFITM1

Hs.147674
2
319
808
232099_at3
232099_at
6 4 2 0 0 4 4 6 5 4 6 3 1 1 1
Homo sapiens protocadherin beta 16 (PCDHB16), mRNA /cds=(1155,3
http://intranet.metagen.de/c gi-bin/eike/prob eset_anno/pr obeset_anno. pl?probeset_i d=232099_at &chip_id=3 http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=14 7674 http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=14 7674 http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=14 7674
485) /gb=NM_020 957 /gi=14195604 /ug=Hs.1476 74 /len=4827
Hs.147674
protocadherin beta 16 PCDHB16

Hs.152292	2	320	809	203874_s_at2	**203874_s_at**	5	5	3	0	0	0	389	279	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203874_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152292	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152292	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1), mRNA /cds=(141,3071) /gb=NM_003069 /gi=4507066 /ug=Hs.152292 /len=3634	Hs.152292	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	SMARCA1

Hs.152292	2	320,2	809,2	203874_s_at2	**203874_s_at**	5	5	3	0	0	0	389	279	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203874_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152292	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152292	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1), mRNA /cds=(141,3071) /gb=NM_003069 /gi=4507066 /ug=Hs.152292 /len=3634	Hs.152292

SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
SMARCA1

Hs.152931	2	321	810	201795_at2	**201795_at**	2	0	0	0	0	0	314	908	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201795_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152931	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=152931	Homo sapiens lamin B receptor (LBR), mRNA /cds=(75,1922) /gb=NM_002296 /gi=4504960 /ug=Hs.152931 /len=3714	Hs.152931	lamin B receptor LBR

Hs.153752	2	322	811	201853_s_at2	**201853_s_at**	7	4	2	0	0	0	121	442	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201853_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=153752	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=153752	Homo sapiens cell division cycle 25B (CDC25B), transcript variant 4, mRNA /cds=(222,2027) /gb=NM_021874 /gi=11641414 /ug=Hs.153752 /len=3195	Hs.153752	cell division cycle 25B	CDC25B

Hs.153792	2	323	812	203200_s_at2	**203200_s_at**	4	2	0	0	0	0	147	655	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203200_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=153792	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=153792	Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(30,2207) /gb=NM_024010 /gi=13325067 /ug=Hs.153792 /len=3291	Hs.153792	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	MTRR

Hs.155227	2	324	813	202894_at2	**202894_at**	6	3	2	0	0	2	231	437	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202894_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155227	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155227	Homo sapiens EphB4 (EPHB4), mRNA /cds=(85,3048) /gb=NM_004444 /gi=17975769 /ug=Hs.155227 /len=3945	Hs.155227	EphB4 EPHB4

Hs.155356	2	325	814	203545_at2	**203545_at**	5	2	0	0	0	0	132	434	2	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203545_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155356	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=155356	Homo sapiens hypothetical protein MGC2840 similar to a putative glucosyltransferase (MGC2840), mRNA /cds=(57,1637) /gb=NM_024079 /gi=13129069 /ug=Hs.155356 /len=1675	Hs.155356	hypothetical protein MGC2840 similar to a putative glucosyltransferase	MGC2840
Hs.15898	2	326	815	219664_s_at2	**219664_s_at**	7	3	0	0	0	0	270	302	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219664_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=15898	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=15898	Homo sapiens 2,4-dienoyl CoA reductase 2, peroxisomal (DECR2), mRNA /cds=(21,899) /gb=NM_020664 /gi=10190703 /ug=Hs.15898 /len=1498	Hs.15898	2,4-dienoyl CoA reductase 2, peroxisomal	DECR2

Hs.16165	2	327	816	204328_at2	**204328_at**	7	1	0	0	0	0	415	411	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204328_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=16165	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=16165	Homo sapiens expressed in activated T/LAK lymphocytes (LAK-4P), mRNA /cds=(52,1386) /gb=NM_007267 /gi=7305226 /ug=Hs.16165 /len=1639	Hs.16165	expressed in activated T/LAK lymphocytes LAK-4P

Hs.1624	2	328	817	202023_at2	**202023_at**	6	4	2	0	0	1	567	573	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202023_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1624	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1624	Homo sapiens ephrin-A1 (EFNA1), mRNA /cds=(73,690) /gb=NM_004428 /gi=4758245 /ug=Hs.1624 /len=1480	Hs.1624	ephrin-A1 EFNA1

Hs.16530	2	329	818	209924_at2	**209924_at**	5	4	4	3	2	2	640	671	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209924_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=16530	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=16530	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated (SCYA18), mRNA /cds=(70,339) /gb=NM_002988 /gi=4506830 /ug=Hs.16530 /len=803	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated	SCYA18

Hs.168383	2	330	819	202638_s_at2	**202638_s_at**	6	5	4	1	2	3	724	1065	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202638_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=168383	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=168383

Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1), mRNA /cds=(57,1655) /gb=NM_000201 /gi=4557877 /ug=Hs.168383 /len=2986

Hs.168383

intercellular adhesion molecule 1 (CD54), human rhinovirus receptor

ICAM1

Hs.169401	2	331	820	203382_s_at2	**203382_s_at**	2	2	2	2	0	10	579	227	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203382_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169401	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169401	Homo sapiens apolipoprotein E (APOE), mRNA /cds=(60,1013) /gb=NM_000041 /gi=4557324 /ug=Hs.169401 /len=1156	Hs.169401	apolipoprotein E	APOE

Hs.169857	2	332	821	201876_at2	**201876_at**	6	3	1	0	0	0	267	565	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201876_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169857	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169857	Homo sapiens paraoxonase 2 (PON2), mRNA /cds=(32,1096) /gb=NM_000305 /gi=4505952 /ug=Hs.169857 /len=1600	Hs.169857	paraoxonase 2 PON2

Hs.169939	2	333	822	203283_s_at2	**203283_s_at**	5	4	3	0	0	1	408	891	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203283_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169939	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=169939	Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), mRNA /cds=(358,1428) /gb=NM_012262 /gi=12545388 /ug=Hs.169939 /len=6708	Hs.169939	heparan sulfate 2-O-sulfotransferase 1	HS2ST1

Hs.170279	2	334	823	210665_at2	**210665_at**	4	4	2	2	2	1	705	927	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210665_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=170279	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=170279	Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(0,914) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915	Hs.170279	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	TFPI

Hs.172199	2	335	824	203741_s_at2	**203741_s_at**	10	6	4	0	0	1	482	194	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203741_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=172199	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=172199	Homo sapiens adenylate cyclase 7 (ADCY7), mRNA /cds=(265,3507) /gb=NM_001114 /gi=4557254 /ug=Hs.172199 /len=6196	Hs.172199	adenylate cyclase 7 ADCY7
Hs.172788	2	336	825	217858_s_at2	**217858_s_at**	4	3	2	0	0	0	317	666	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217858_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=172788	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=172788	Homo sapiens ALEX3 protein (ALEX3), mRNA /cds=(480,1619) /gb=NM_016607 /gi=7705273 /ug=Hs.172788 /len=2025	Hs.172788	ALEX3 protein ALEX3

Hs.173736	2	337	826	220525_s_at2	**220525_s_at**	5	1	0	0	0	0	335	459	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=220525_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=173736	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=173736	Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA /cds=(68,1498) /gb=NM_012103 /gi=6912259 /ug=Hs.173736 /len=1664	Hs.173736	ancient ubiquitous protein 1 AUP1

Hs.180383	2	338	827	208891_at2	**208891_at**	6	4	3	0	2	0	411	476	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208891_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=180383	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=180383	Homo sapiens dual specificity phosphatase 6 (DUSP6), transcript variant 1, mRNA /cds=(351,1496) /gb=NM_001946 /gi=4503418 /ug=Hs.180383 /len=2390	Hs.180383	dual specificity phosphatase 6	DUSP6

Hs.18069	2	339	828	201212_at2	**201212_at**	5	1	1	0	0	0	81	611	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201212_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=18069	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=18069	Homo sapiens, protease, cysteine, 1 (legumain), clone MGC:15832 IMAGE:3507728, mRNA, complete cds /cds=(1124,2425) /gb=BC008004 /gi=14124955 /ug=Hs.18069 /len=2979	Hs.18069	legumain	LGMN

Hs.180878	2	340	829	203549_s_at2	**203549_s_at**	6	5	3	2	1	1	524	705	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203549_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=180878	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=180878	Homo sapiens lipoprotein lipase (LPL), mRNA /cds=(174,1601) /gb=NM_000237 /gi=4557726 /ug=Hs.180878 /len=3549	Hs.180878	lipoprotein lipase	LPL

Hs.181286	2	341	830	206239_s_at2	**206239_s_at**	9	8	8	7	1	1	198	3	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206239_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=181286	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=181286	Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), mRNA /cds=(60,299) /gb=NM_003122 /gi=4507178 /ug=Hs.181286 /len=368	Hs.181286

serine protease inhibitor, Kazal type 1
SPINK1

Hs.182591	2	342	831	205590_at2	**205590_at**	5	4	2	0	0	1	520	974	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205590_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182591	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182591	Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA /cds=(103,2496) /gb=NM_005739 /gi=6382080 /ug=Hs.182591 /len=5021	Hs.182591	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	RASGRP1

Hs.182874	2	343	832	221737_at2	**221737_at**	7	3	1	0	0	1	339	599	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=221737_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182874	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=182874	Homo sapiens cDNA: FLJ21929 fis, clone HEP04272 /cds=UNKNOWN /gb=AK025582 /gi=10438141 /ug=Hs.182874 /len=2941	Hs.182874	guanine nucleotide binding protein (G protein) alpha 12	GNA12

Hs.183648
2
344
833
202066_at2
202066_at
5 2 0 0 0 0 0 0
154
653
2 1
1
&chip_id=2 3648 3648 48 /len=4313
d=202066_at =Hs&CID=18 =Hs&CID=18 /ug=Hs.1836
pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=4505982
obeset_anno. v/UniGene/cl v/UniGene/cl 626
eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_003
bin/eike/prob http://www.nc http://www.nc 37)
gi-
metagen.de/c
http://intranet.
/cds=(229,38
mRNA
1 (PPFIA1),
(liprin), alpha
protein
interacting
(PTPRF),
f polypeptide
phosphatase,
receptor type,
tyrosine
protein
sapiens
Homo

Hs.183648
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
PPFIA1

Hs.183858	2	345	834	213301_x_at2	**213301_x_at**	7	2	1	0	0	0	403	385	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213301_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=183858	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=183858	Homo sapiens transcriptional intermediary factor 1 (TIF1), mRNA /cds=(116,3163) /gb=NM_003852 /gi=14971414 /ug=Hs.183858 /len=3803	Hs.183858	transcriptional intermediary factor 1 TIF1

Hs.184011	2	346	835	217848_s_at2	**217848_s_at**	5	2	0	0	0	0	307	596	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217848_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184011	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184011	Homo sapiens pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,946) /gb=NM_021129 /gi=11056043 /ug=Hs.184011 /len=1282	Hs.184011	pyrophosphatase (inorganic) PP
Hs.184465	2	347	836	218627_at2	**218627_at**	5	2	1	1	0	0	338	413	2	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218627_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184465	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=184465	Homo sapiens hypothetical protein FLJ11259 (FLJ11259), mRNA /cds=(87,485) /gb=NM_018370 /gi=8922957 /ug=Hs.184465 /len=2835	Hs.184465	hypothetical protein FLJ11259 FLJ11259

Hs.1872	2	348	837	208383_s_at2	**208383_s_at**	3	3	3	3	0	9	563	946	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208383_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1872	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=1872	Homo sapiens phosphoenolpyruvate carboxykinase 1 (soluble) (PCK1), mRNA /cds=(121,1989) /gb=NM_002591 /gi=4505638 /ug=Hs.1872 /len=2657	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble) PCK1

Hs.194691

2	350	839	203108_at2	**203108_at**	6	5	3	2	2	0	4	59	222	2	1	1
																http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=203108_at&chip_id=2
																Homo sapiens retinoic acid induced 3 (RAI3), mRNA /cds=(253,13 26) /gb=NM_003979 /gi=12056470 /ug=Hs.194691 retinoic acid induced 3 RAI3
																4691 91 /len=2456

Hs.190161

2	349	838	220532_s_at2	**220532_s_at**	4	3	1	0	2	4	636	333	2	1	1
															http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=220532_s_at&chip_id=2
															Homo sapiens LR8 protein (LR8), mRNA /cds=(163,97 5) /gb=NM_014020 /gi=7662497 /ug=Hs.190161 LR8 protein LR8
															0161 61 /len=1208

Hs.194710	2	351	840	219508_at2	**219508_at**	5	4	3	2	2	0	729	448	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219508_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194710	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=194710	Homo sapiens glucosaminyl (N-acetyl) transferase 3, mucin type (GCNT3), mRNA /cds=(353,1669) /gb=NM_004751 /gi=4758421 /ug=Hs.194710 /len=2128	Hs.194710

- glucosaminyl (N-acetyl) transferase 3, mucin type GCNT3

Hs.20450	2	352	841	219386_s_at2	**219386_s_at**	4	4	2	0	0	4	656	1058	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219386_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20450	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20450	Homo sapiens BCM-like membrane protein precursor (BLAME), mRNA /cds=(88,945) /gb=NM_020125 /gi=9910341 /ug=Hs.20450 /len=3197	Hs.20450	B lymphocyte activator macrophage expressed BLAME

Hs.20716	2	353	842	215171_s_at2	**215171_s_at**	4	0	0	0	0	0	93	769	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215171_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20716	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=20716	Homo sapiens translocase of inner mitochondrial membrane 17 homolog A (yeast) (TIMM17A), mRNA /cds=(7,522) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	Hs.20716	translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A

Hs.207776	2	354	843	204333_s_at2	**204333_s_at**	7	4	4	0	0	0	392	351	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204333_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=207776	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=207776	Homo sapiens aspartylglucosaminidase (AGA), mRNA /cds=(170,1210) /gb=NM_000027 /gi=4557272 /ug=Hs.207776 /len=2150	Hs.207776	aspartylglucosaminidase	AGA

Hs.211580	2	355	844	206247_at2	**206247_at**	8	7	5	2	0	2	323	110	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206247_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211580	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211580	Homo sapiens MHC class I polypeptide-related sequence B (MICB), mRNA /cds=(5,1156) /gb=NM_005931 /gi=5174564 /ug=Hs.211580 /len=2367	Hs.211580	MHC class I polypeptide-related sequence B MICB

Hs.211587	2	356	845	210145_at2	**210145_at**	7	5	3	3	0	1	427	126	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210145_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211587	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=211587	Homo sapiens phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds /cds=(138,2387) /gb=M68874 /gi=190003 /ug=Hs.211587 /len=2875	Hs.211587	phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A

Hs.215766	2	357	846	218239_s_at2	**218239_s_at**	7	0	0	0	0	0	90	660	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218239_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=215766	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=215766	Homo sapiens G protein-binding protein CRFG (CRFG), mRNA /cds=(23,1924) /gb=NM_012341 /gi=6912531 /ug=Hs.215766 /len=2414	Hs.215766	G protein-binding protein CRFG	CRFG
Hs.220529	2	358	847	201884_at2	**201884_at**	6	5	4	2	2	2	971	283	2	1	1		http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201884_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=220529	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=220529	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 5 (CEACAM5), mRNA /cds=(114,2222) /gb=NM_004363 /gi=11386170 /ug=Hs.220529 /len=2974	Hs.220529	carcinoembryonic antigen-related cell adhesion molecule 5	CEACAM5

Hs.2210	2	359	848	225947_at3	**225947_at**	4	1	0	0	0	0	273	493	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225947_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2210	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2210	Homo sapiens mRNA; cDNA DKFZp434E0727 (from clone DKFZp434E0727) /cds=UNKNOWN /gb=AL133017 /gi=6453497 /ug=Hs.2210 /len=4249	Hs.2210	thyroid hormone receptor interactor 3	TRIP3
Hs.22151	2	360	849	225943_at3	**225943_at**	8	0	0	0	0	3	20	402	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=225943_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22151	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=22151	Homo sapiens mRNA for KIAA1226 protein, partial cds /cds=UNKNOWN /gb=AB033052 /gi=6330675 /ug=Hs.22151 /len=5343	Hs.22151	neurolysin (metallopeptidase M3 family)	NLN

Hs.23590	2	361	850	205234_at2	**205234_at**	7	7	6	5	1	4	338	74	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205234_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23590	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23590	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4), mRNA /cds=(182,1645) /gb=NM_004696 /gi=4759113 /ug=Hs.23590 /len=2529	Hs.23590	ESTs

ODZ1

odz, odd Oz/ten-m homolog 1(Drosophila)

Hs.23796

Homo sapiens odz, odd Oz/ten-m homolog 1(Drosophila) (ODZ1), mRNA /cds=(64,824

gi-

http://intranet.metagen.de/cbin/eike/probeset_anno/probeset_info.pl?probeset_id=205728_at&chip_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=23

/gb=NM_014253

/gi=7657410

/ug=Hs.23796

6 /len=8297

796

796

1

205728_at

Hs.23796

2

362

851

205728_at2

205728_at

5 4 3 2 0 7 666 952 2 1

Hs.238272	2	363	852	202660_at2	**202660_at**	7	4	2	1	0	0	631	310	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202660_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=238272	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=238272	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA /cds=(418,8523) /gb=NM_002223 /gi=4504792 /ug=Hs.238272 /len=10524	Hs.238272	inositol 1,4,5-triphosphate receptor, type 2 ITPR2

Hs.239760	2	364	853	208660_at2	**208660_at**	6	2	0	0	0	4	53	404	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208660_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239760	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=239760	Homo sapiens, clone MGC:19593 IMAGE:3542491, mRNA, complete cds /cds=(118,1518) /gb=BC010106 /gi=14603294 /ug=Hs.239760 /len=2900	Hs.239760	citrate synthase	CS
Hs.24048	2	365	854	219117_s_at2	**219117_s_at**	5	4	3	0	2	0	847	295	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219117_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24048	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24048	Homo sapiens FK506 binding protein precursor (LOC51303), mRNA /cds=(72,677) /gb=NM_016594 /gi=7706130 /ug=Hs.24048 /len=727	Hs.24048	FK506 binding protein precursor	LOC51303

Hs.241515	2	366	855	211727_s_at2	**211727_s_at**	6	2	2	0	1	0	225	580	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211727_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241515	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=241515	Homo sapiens COX11 homolog, cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(47,877) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	Hs.241515	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	COX11

Hs.24678	2	367	856	223391_at3	**223391_at**	7	4	2	1	0	1	374	231	3	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223391_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24678	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=24678	Homo sapiens sphingosine-1-phosphatase (LOC81537), mRNA /cds=(32,1357) /gb=NM_030791 /gi=13540568 /ug=Hs.24678 /len=2258	Hs.24678	sphingosine-1-phosphatase LOC81537
Hs.247964	2	368	857	215536_at2	**215536_at**	4	4	4	1	2	4	715	1343	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215536_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=247964	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=247964	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes /cds=(0,794) /gb=X87344 /gi=1054740 /ug=Hs.247964 /len=795	Hs.247964	

Hs.251531	2	369	858	203396_at2	**203396_at**	0	0	0	0	0	0	161	1016	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203396_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=251531	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=251531	Homo sapiens cDNA FLJ31152 fis, clone IMR322001584, highly similar to PROTEASOME COMPONENT C9 (EC 3.4.99.46) /cds=UNKNOWN /gb=AK055714 /gi=16550510 /ug=Hs.251531 /len=2743	Hs.251531	proteasome (prosome, macropain) subunit, alpha type, 4	PSMA4

Hs.251673	2	370	859	220668_s_at2	**220668_s_at**	4	1	0	0	0	6	143	631	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=220668_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=251673	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=251673	Homo sapiens DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), mRNA /cds=(114,2675) /gb=NM_006892 /gi=5901939 /ug=Hs.251673 /len=4145	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 beta DNMT3B

Hs.25333	2	371	860	205403_at2	**205403_at**	4	4	4	1	3	4	1053	1292	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205403_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25333	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25333	Homo sapiens interleukin 1 receptor, type II (IL1R2), mRNA /cds=(61,1257) /gb=NM_004633 /gi=4758597 /ug=Hs.25333 /len=1286	Hs.25333	interleukin 1 receptor, type II	IL1R2

Hs.25829	2	372	861	223467_at3	**223467_at**	6	4	2	0	1	3	672	689	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223467_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25829	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=25829	Homo sapiens RAS, dexamethasone-induced 1 (RASD1), mRNA /cds=(0,845) /gb=NM_016084 /gi=7706358 /ug=Hs.25829 /len=1187	Hs.25829	RAS, dexamethasone-induced 1	RASD1

Hs.261023	2	373	862	220094_s_at2	**220094_s_at**	6	3	1	0	0	0	221	431	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=220094_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=261023	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=261023	Homo sapiens hypothetical protein FLJ20958 (FLJ20958), mRNA /cds=(140,913) /gb=NM_022102 /gi=13430855 /ug=Hs.261023 /len=1842	Hs.261023	hypothetical protein FLJ20958 FLJ20958

Hs.266470
2
374
863
231725_a13
231725_at
8 7 2 1 0 3 160 128 3 1

1

&chip_id=3 6470 6470 70 /len=2733
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pl?probeset_i ust.cgi?ORG ust.cgi?ORG /gi=14195608
obeset_anno. v/UniGene/cl v/UniGene/cl 936
eset_anno/pr bi.nlm.nih.go bi.nlm.nih.go /gb=NM_018
bin/eike/prob http://www.nc http://www.nc 34)
gi-
metagen.de/c
http://intranet.

/cds=(138,25
mRNA
(PCDHB2),
beta 2
protocadherin
sapiens
Homo

Hs.266470
protocadherin beta 2
PCDHB2

Hs.267566	2	375	864	219316_s_at2	**219316_s_at**	4	1	1	0	0	8	3	305	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219316_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=267566	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=267566	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA /cds=(324,1904) /gb=NM_017791 /gi=8923349 /ug=Hs.267566 /len=3614	Hs.267566	hypothetical protein FLJ20371 FLJ20371

Hs.2707	2	376	865	215438_x_at2	**215438_x_at**	4	1	0	0	0	0	308	798	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215438_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2707	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=2707	Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA /cds=(648,2147) /gb=NM_002094 /gi=4504166 /ug=Hs.2707 /len=2587	Hs.2707	G1 to S phase transition 1	GSPT1

Hs.270833	2	377	866	205239_at2	**205239_at**	6	5	3	1	5	0	858	1032	2	1	1	1	http://intranet. metagen.de/c gi- bin/eike/prob eset_anno/pr obeset_anno. pl?probeset_i d=205239_at &chip_id=2	http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=27 0833	http://www.nc bi.nlm.nih.go v/UniGene/cl ust.cgi?ORG =Hs&CID=27 0833	Homo sapiens amphiregulin (schwannom a-derived growth factor) (AREG), mRNA /cds=(209,96 7) /gb=NM_001 657 /gi=4502198 /ug=Hs.2708 33 /len=1230	Hs.270833	amphiregulin (schwannoma-derived growth factor)	AREG

Hs.270956	2	378	867	229500_at3	**229500_at**	8	2	1	0	0	1	166	361	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=229500_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=270956	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=270956	Homo sapiens chromosome 4 open reading frame 1 (C4orf1), mRNA /cds=(120,1826) /gb=NM_006345 /gi=7656945 /ug=Hs.270956 /len=3250	Hs.270956	chromosome 4 open reading frame 1	C4orf1

Hs.271752	2	379	868	232103_at3	**232103_at**	5	2	0	0	0	0	519	422	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=232103_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271752	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=271752	Homo sapiens 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1), mRNA /cds=(113,1039) /gb=NM_006085 /gi=5174398 /ug=Hs.271752 /len=2113	Hs.271752	3'(2'), 5'-bisphosphate nucleotidase 1 BPNT1

Hs.274230	2	380	869	203060_s_at2	**203060_s_at**	7	4	4	1	2	2	569	462	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203060_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274230	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274230	Homo sapiens PAPS synthetase-2 (PAPSS2) mRNA, complete cds /cds=(63,1907) /gb=AF074331 /gi=5052074 /ug=Hs.274230 /len=3774	Hs.274230	3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2

Hs.274351	2	381	870	222451_s_at3	**222451_s_at**	9	3	3	1	0	1	162	224	3	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222451_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274351	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274351	Homo sapiens mRNA; cDNA DKFZp761E1347 (from clone DKFZp761E1347); partial cds /cds=UNKNOWN /gb=AL161962 /gi=7328016 /ug=Hs.274351 /len=2866	Hs.274351	zinc finger, DHHC domain containing 9	ZDHHC9
Hs.274407	2	382	871	208165_s_at2	**208165_s_at**	5	4	2	1	0	4	521	581	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208165_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274407	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=274407	Homo sapiens protease, serine, 16 (thymus) (PRSS16), mRNA /cds=(12,1556) /gb=NM_005865 /gi=5031992 /ug=Hs.274407 /len=2699	Hs.274407	protease, serine, 16 (thymus)	PRSS16

Hs.27747

2

383

872

209631_s_at2

209631_s_at

5 4 4 3 0 6 9 2 1 1 1

584

945

1 1

http://intranet.	Human
metagen.de/c	putative
gi-	endothelin
bin/elke/prob	receptor type
eset_anno/pr	B-like protein
obeset_anno.	mRNA,
pl?probeset_i	complete cds
d=209631_s_	
at&chip_id=2	

http://www.nc /cds=(1778,3
bi.nlm.nih.go 619)
v/UniGene/cl /gb=U87460
ust.cgi?ORG /gi=2076881
=Hs&CID=27 /ug=Hs.2774.
747 7 /len=4156

Hs.27747

G protein-coupled receptor 37 (endothelin receptor type B-like)

GPR37

Hs.279884	2	384	873	218435_at2	**218435_at**	5	4	3	0	0	0	542	1039	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218435_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279884	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279884	Homo sapiens DNAJ domain-containing (MCJ), mRNA /cds=(423,875) /gb=NM_013238 /gi=7019452 /ug=Hs.279884 /len=1074	Hs.279884	DNAJ domain-containing	MCJ

Hs.279926	2	385	874	224392_s_at3	**224392_s_at**	9	8	4	2	0	1	209	108	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=224392_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279926	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=279926	Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), mRNA /cds=(55,1266) /gb=NM_014322 /gi=7657070 /ug=Hs.279926 /len=2110	Hs.279926	opsin 3 (encephalopsin, panopsin)	OPN3

Hs.283022	2	386	875	219434_at2	**219434_at**	4	2	1	0	0	1	341	503	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219434_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283022	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283022	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751) /gb=NM_018643 /gi=8924261 /ug=Hs.283022 /len=884	Hs.283022	triggering receptor expressed on myeloid cells 1 TREM1

Hs.283664	2	387	876	209135_at2	**209135_at**	8	2	0	0	1	0	260	465	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209135_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283664	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=283664	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 3, mRNA /cds=(11,952) /gb=NM_032466 /gi=14589859 /ug=Hs.283664 /len=2680	Hs.283664	aspartate beta-hydroxylase	ASPH

Hs.284296	2	388	877	222977_at3	**222977_at**	9	3	0	0	0	0	287	253	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222977_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284296	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 /cds=UNKNOWN /gb=AK026646 /gi=10439543 /ug=Hs.284296 /len=1741	Hs.284296	surfeit 4	SURF4

Hs.284380	2	389	878	211417_x_at2	**211417_x_at**	4	4	2	0	0	4	609	806	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211417_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284380	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=284380	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 2, mRNA /cds=(669,2378) /gb=NM_013421 /gi=9845490 /ug=Hs.284380 /len=2535	Hs.284380	gamma-glutamyltransferase 1 GGT1

Hs.285976	2	390	879	222212_s_at2	**222212_s_at**	7	3	1	0	1	0	295	560	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222212_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285976	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=285976	Homo sapiens LAG1 longevity assurance homolog 2 (S. cerevisiae) (LASS2), mRNA /cds=(49,741) /gb=NM_013384 /gi=9937997 /ug=Hs.285976 /len=1646	Hs.285976	LAG1 longevity assurance homolog 2 (S. cerevisiae)	LASS2

Hs.288031	2	391	880	211423_s_at2	**211423_s_at**	6	4	3	0	0	0	442	517	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211423_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288031	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288031	Homo sapiens sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like (SC5DL), mRNA /cds=(48,947) /gb=NM_006918 /gi=10800413 /ug=Hs.288031 /len=2092	Hs.288031	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	SC5DL

Hs.288057	2	392	881	218017_s_at2	**218017_s_at**	4	3	3	0	0	0	569	422	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218017_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288057	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288057	Homo sapiens hypothetical protein FLJ22242 (FLJ22242), mRNA /cds=(250,870) /gb=NM_025070 /gi=13376612 /ug=Hs.288057 /len=1300	Hs.288057	hypothetical protein FLJ22242 FLJ22242
Hs.288126	2	393	882	218638_s_at2	**218638_s_at**	5	4	4	0	3	1	758	1273	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218638_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288126	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288126	Homo sapiens spondin 2, extracellular matrix protein (SPON2), mRNA /cds=(275,1270) /gb=NM_012445 /gi=6912681 /ug=Hs.288126 /len=1807	Hs.288126	spondin 2, extracellular matrix protein SPON2

Hs.288817	2	394	883	227614_at3	**227614_at**	5	2	2	0	0	6	324	302	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=227614_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288817	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=288817	Homo sapiens, clone IMAGE:4563921, mRNA, partial cds /cds=UNKNOWN /gb=BC012337 /gi=15214422 /ug=Hs.288817 /len=2868	Hs.288817	hypothetical protein FLJ22761	FLJ22761

Hs.289101	2	395	884	208612_at2	**208612_at**	4	4	2	0	0	0	492	533	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208612_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289101	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=289101	Homo sapiens glucose regulated protein, 58kD (GRP58), mRNA /cds=(0,1517) /gb=NM_005313 /gi=4885358 /ug=Hs.289101 /len=1518	Hs.289101	glucose regulated protein, 58kD GRP58

Hs.28914	2	396	885	203219_s_at2	**203219_s_at**	7	4	1	0	0	1	450	431	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203219_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28914	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=28914	Homo sapiens adenine phosphoribosyltransferase (APRT), mRNA /cds=(71,613) /gb=NM_000485 /gi=4502170 /ug=Hs.28914 /len=841	Hs.28914	adenine phosphoribosyltransferase	APRT

Hs.295944	2	397	886	209277_at2	**209277_at**	5	4	4	2	3	0	575	648	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209277_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=295944	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=295944	Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), mRNA /cds=(56,763) /gb=NM_006528 /gi=5730090 /ug=Hs.295944 /len=1142	Hs.295944	tissue factor pathway inhibitor 2	TFPI2

Hs.302117

Human DNA sequence from clone RP4-781L3 on chromosome 1p34.3-36.11 Contains a pseudogene similar to IFITM3 (interferon inducedntran smembrane protein 3 (1-8U)), STSs and GSSs

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=2

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30

/cds=(0,401) /gb=AL12199 4 /gi=8648917 /ug=Hs.302117 17 /len=402

1

2117

2117

2 1

415

556

3 3 2 1 0 3

887

398

2

216565_x_at2

216565_x_at

Hs.30464	2	399	888	205034_at2	**205034_at**	8	2	0	0	0	2	124	297	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205034_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30464	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=30464	Homo sapiens cyclin E2 (CCNE2), transcript variant 1, mRNA /cds=(109,1323) /gb=NM_057749 /gi=17318564 /ug=Hs.30464 /len=2748	Hs.30464	cyclin E2	CCNE2

Hs.31137	2	400	889	221840_at2	**221840_at**	6	5	2	0	0	0	393	365	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=221840_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31137	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=31137	Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), mRNA /cds=(51,2153) /gb=NM_006504 /gi=5729992 /ug=Hs.31137 /len=2160	Hs.31137	protein tyrosine phosphatase, receptor type, E	PTPRE

Hs.321579	2	401	890	204087_s_at2	**204087_s_at**	1	0	0	0	0	11	142	819	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204087_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=321579	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=321579	Homo sapiens solute carrier family 5 (sodium-dependent vitamin transporter), member 6 (SLC5A6), mRNA /cds=(391,2298) /gb=NM_021095 /gi=10863878 /ug=Hs.321579 /len=3162	Hs.321579	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	SLC5A6

Hs.322854	2	402	891	223806_s_at3	**223806_s_at**	10	9	9	6	2	0	135	12	3	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223806_s_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=322854	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=322854	Homo sapiens pronapsin A (NAP1), mRNA /cds=(53,1315) /gb=NM_004851 /gi=4758753 /ug=Hs.322854 /len=1438	Hs.322854	pronapsin A NAP1

Hs.323567	2	403	892	201647_s_at2	**201647_s_at**	4	2	0	0	0	1	120	575	2	1			1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201647_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323567	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323567	Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) (CD36L2), mRNA /cds=(251,1687) /gb=NM_005506 /gi=5031630 /ug=Hs.323567 /len=2329	Hs.323567	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) CD36L2

Hs.323769	2	404	893	223020_at3	**223020_at**	4	3	2	0	1	1	428	278	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=223020_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323769	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=323769	Homo sapiens cisplatin resistance related protein CRR9p (CRR9), mRNA /cds=(64,1602) /gb=NM_030782 /gi=18158421 /ug=Hs.323769 /len=2040	Hs.323769	cisplatin resistance related protein CRR9p	CRR9
Hs.325520	2	405	894	208118_x_at2	**208118_x_at**	0	0	0	0	0	12	223	1091	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208118_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=325520	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=325520	Homo sapiens LAT1-3TM protein (LAT1-3TM), mRNA /cds=(79,621) /gb=NM_031211 /gi=13654279 /ug=Hs.325520 /len=2114	Hs.325520	LAT1-3TM protein	LAT1-3TM

Hs.325960	2	406	895	219607_s_at2	**219607_s_at**	5	4	3	1	1	3	763	1027	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219607_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=325960	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=325960	Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4), mRNA /cds=(195,788) /gb=NM_016650 /gi=7706201 /ug=Hs.325960 /len=1076	Hs.325960	membrane-spanning 4-domains, subfamily A, member 4 MS4A4A
Hs.334854	2	407	896	201346_at2	**201346_at**	3	1	0	0	0	3	341	744	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201346_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334854	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=334854	Homo sapiens hypothetical protein FLJ21432 (FLJ21432), mRNA /cds=(109,885) /gb=NM_024551 /gi=13375714 /ug=Hs.334854 /len=3500	Hs.334854	

Hs.336946	2	408	897	215121_x_at2	**215121_x_at**	6	6	6	1	3	0	530	226	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=215121_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=336946	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=336946	Human rearranged immunoglobulin lambda light chain mRNA /cds=(9,710) /gb=X57812 /gi=33723 /ug=Hs.336946 /len=803	Hs.336946
Hs.337616	2	409	898	214582_at2	**214582_at**	5	4	4	1	0	0	510	877	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=214582_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=337616	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=337616	Homo sapiens phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA /cds=(0,3338) /gb=NM_000922 /gi=4505660 /ug=Hs.337616 /len=3339	Hs.337616

Hs.348996	2	410	899	202195_s_at2	**202195_s_at**	6	4	3	0	1	2	501	632	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202195_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348996	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=348996	Homo sapiens, CGI-100 protein, clone MGC:5366 IMAGE:3048959, mRNA, complete cds /cds=(112,801) /gb=BC016556 /gi=16741479 /ug=Hs.348996 /len=3635	Hs.348996
Hs.350470	2	411	900	205009_at2	**205009_at**	4	4	4	2	3	5	993	1342	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205009_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=350470	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=350470	Homo sapiens trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in) (TFF1), mRNA /cds=(40,294) /gb=NM_003225 /gi=4507450 /ug=Hs.350470 /len=540	Hs.350470

Hs.351221	2	412	901	204009_s_at2	**204009_s_at**	4	3	0	0	0	0	299	693	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204009_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351221	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351221	Human K-ras oncogene protein mRNA, complete cds /cds=(192,758) /gb=M54968 /gi=1815608 /ug=Hs.351221 /len=5775	Hs.351221
Hs.351593	2	413	902	205650_s_at2	**205650_s_at**	5	5	3	3	0	7	634	422	2		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205650_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351593	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=351593	Homo sapiens fibrinogen, A alpha polypeptide (FGA), transcript variant alpha-E, mRNA /cds=(30,2630) /gb=NM_000508 /gi=11761627 /ug=Hs.351593 /len=3627	Hs.351593

Hs.352018	2	414	903	202307_s_at2	**202307_s_at**	7	5	4	0	1	1	415	119	2	1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202307_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=352018	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=352018	Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(30,2456) /gb=NM_000593 /gi=9665247 /ug=Hs.352018 /len=2824	Hs.352018
Hs.352341	2	415	904	202558_s_at2	**202558_s_at**	7	5	3	1	0	0	284	205	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202558_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=352341	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=352341	Homo sapiens stress 70 protein chaperone, microsome-associated, 60kD (STCH), mRNA /cds=(36,1451) /gb=NM_006948 /gi=5902125 /ug=Hs.352341 /len=2228	Hs.352341

Hs.37058	2	416	905	210727_at2	**210727_at**	3	3	3	3	0	9	693	1563	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210727_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=37058	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=37058	Homo sapiens calcitonin/calcitonin-related polypeptide, alpha (CALCA), mRNA /cds=(70,495) /gb=NM_001741 /gi=4502544 /ug=Hs.37058 /len=791	Hs.37058

calcitonin/calcitonin-related polypeptide, alpha

CALCA

Hs.41143	2	417	906	213222_at2	**213222_at**	9	5	4	2	0	0	413	88	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213222_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41143	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41143	Homo sapiens mRNA for KIAA0581 protein, partial cds /cds=UNKNOWN /gb=AB011153 /gi=3043685 /ug=Hs.41143 /len=5147	Hs.41143	phospholipase C, beta 1 (phosphoinositide-specific) PLCB1

Hs.41270	2	418	907	202620_s_at2	**202620_s_at**	8	4	4	0	1	0	66	215	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202620_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41270	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=41270	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA /cds=(0,2213) /gb=NM_000935 /gi=4505888 /ug=Hs.41270 /len=3503	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	PLOD2

Hs.4147	2	419	908	201399_s_at2	**201399_s_at**	6	5	2	0	0	1	266	249	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201399_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=4147	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=4147	Homo sapiens, translocating chain-associating membrane protein, clone MGC:784 IMAGE:3347823, mRNA, complete cds /cds=(91,1215) /gb=BC000687 /gi=12653796 /ug=Hs.4147 /len=2722	Hs.4147

translocating chain-associating membrane protein
TRAM

Hs.42194

2

420

909

222753_s_at3

222753_s_at

5 3 1 0 0 2 413 282 3 1

1 1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=222753_s_at&chip_id=3

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=42194

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=42194

/gb=NM_021928 /gi=11345461 /ug=Hs.42194 /len=1544

Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22/23 (FLJ22649), mRNA /cds=(113,655)

Hs.42194

hypothetical protein FLJ22649 similar to signal peptidase SPC22/23 FLJ22649

Hs.42331	2	421	910	205107_s_at2	**205107_s_at**	6	1	0	0	1	5	342	403	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205107_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=42331	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=42331	Homo sapiens ephrin-A4 (EFNA4), mRNA /cds=(27,632) /gb=NM_005227 /gi=4885196 /ug=Hs.42331 /len=1181	Hs.42331	ephrin-A4	EFNA4

Hs.429	2	422	911	207508_at2	**207508_at**	2	0	0	0	0	0	264	712	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=207508_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=429	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=429	Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(254,682) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	ATP5G3

Hs.44197	2	423	912	213094_at2	**213094_at**	5	4	3	2	4	0	906	537	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213094_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44197	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44197	Homo sapiens cDNA FLJ14937 fis, clone PLACE1010231, weakly similar to CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR /cds=(192,1730) /gb=AK027843 /gi=14042817 /ug=Hs.44197 /len=3088	Hs.44197	hypothetical protein DKFZp564D0462	DKFZP564D0462

Hs.44563	2	424	913	213379_at2	**213379_at**	5	3	0	0	0	0	291	523	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213379_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44563	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44563	Homo sapiens, clone MGC:22534 IMAGE:4696019, mRNA, complete cds /cds=(47,1162) /gb=BC020728 /gi=18088423 /ug=Hs.44563 /len=1566	Hs.44563	hypothetical protein CL640	CL640

Hs.44926	2	425	914	203716_s_at2	**203716_s_at**	3	3	2	2	0	9	414	438	2	1	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203716_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44926	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=44926	Homo sapiens dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) (DPP4), mRNA /cds=(75,2375) /gb=NM_001935 /gi=4503366 /ug=Hs.44926 /len=3407	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) DPP4

Hs.46784	2	426	915	219287_at2	**219287_at**	4	4	3	2	0	0	579	888	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219287_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=46784	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=46784	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 4 (KCNMB4), mRNA /cds=(60,692) /gb=NM_014505 /gi=15100165 /ug=Hs.46784 /len=1181

Hs.46784

potassium large conductance calcium-activated channel, subfamily M, beta member 4

KCNMB4

Hs.47584	2	427	916	205968_at2	**205968_at**	8	5	1	1	0	3	344	170	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205968_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=47584	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=47584	Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA /cds=(131,1606) /gb=NM_002252 /gi=4504862 /ug=Hs.47584 /len=2097	Hs.47584	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	KCNS3

Hs.50477

2

428

917

210951_x_at2

210951_x_at

8 4 2 0 1 0 136 213 2 1 1

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=210951_x_at&chip_id=2

Homo sapiens Rab27a mRNA, complete cds

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=50 477

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=50 477

/cds=(245,911)

/gb=U38654

/gi=4887230

/ug=Hs.50477

7 /len=2496

Hs.50477

RAB27A, member RAS oncogene family

RAB27A

Hs.50649	2	429	918	210609_s_at2	**210609_s_at**	7	4	4	2	1	1	380	371	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210609_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=50649	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=50649	Homo sapiens quinone oxidoreductase homolog (PIG3), mRNA /cds=(527,1495) /gb=NM_004881 /gi=4758911 /ug=Hs.50649 /len=1670	Hs.50649	quinone oxidoreductase homolog PIG3

Hs.530	2	430	919	222073_at2	**222073_at**	5	4	3	2	4	0	696	1493	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222073_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=530	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=530	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA /cds=(161,5173) /gb=NM_000091 /gi=14165440 /ug=Hs.530 /len=8050	Hs.530	collagen, type IV, alpha 3 (Goodpasture antigen)	COL4A3

Hs.5753	2	431	920	203126_at2	**203126_at**	4	2	1	0	0	0	545	340	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203126_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5753	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5753	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA /cds=(214,1080) /gb=NM_014214 /gi=7657235 /ug=Hs.5753 /len=1500	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2 IMPA2

Hs.57553	2	432	921	212997_s_at2	**212997_s_at**	2	1	0	0	0	3	142	954	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212997_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=57553	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=57553	Homo sapiens tousled-like kinase 2 (TLK2), mRNA /cds=(146,2395) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327	Hs.57553	tousled-like kinase 2 TLK2

Hs.5831	2	433	922	201666_at2	**201666_at**	5	4	3	0	0	4	644	880	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201666_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5831	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=5831	Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA /cds=(62,685) /gb=NM_003254 /gi=4507508 /ug=Hs.5831 /len=782	Hs.5831	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	TIMP1

Hs.59384	2	434	923	213422_s_at2	**213422_s_at**	6	5	1	0	0	1	397	515	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213422_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=59384	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=59384	Homo sapiens hypothetical protein MGC3047 (MGC3047), mRNA /cds=(40,1368) /gb=NM_032348 /gi=14150144 /ug=Hs.59384 /len=2299	Hs.59384	hypothetical protein MGC3047 MGC3047
Hs.6459	2	435	924	218151_x_at2	**218151_x_at**	5	2	1	0	0	3	386	410	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218151_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=6459	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=6459	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA /cds=(239,1576) /gb=NM_024531 /gi=13375681 /ug=Hs.6459 /len=1853	Hs.6459	hypothetical protein FLJ11856 FLJ11856

Hs.69285	2	436	925	210510_s_at2	**210510_s_at**	3	3	3	0	0	9	379	370	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210510_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69285	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=69285	Homo sapiens neuropilin 1 (NRP1), mRNA /cds=(0,2771) /gb=NM_003873 /gi=4505456 /ug=Hs.69285 /len=2772	Hs.69285	neuropilin 1	NRP1

Hs.70337	2	437	926	209030_s_at2	**209030_s_at**	7	4	1	0	0	2	544	452	2	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=209030_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=70337	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=70337	Homo sapiens nectin-like protein 2 (NECL2) mRNA, complete cds /cds=(3,1331) /gb=AF132811 /gi=7767238 /ug=Hs.70337 /len=3512	Hs.70337	immunoglobulin superfamily, member 4	IGSF4
Hs.72289	2	438	927	219215_s_at2	**219215_s_at**	10	5	3	1	0	1	198	165	2	1			1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219215_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=72289	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=72289	Homo sapiens hypothetical protein FLJ20327 (FLJ20327), mRNA /cds=(305,2185) /gb=NM_017767 /gi=8923304 /ug=Hs.72289 /len=2317	Hs.72289		

Hs.7331	2	439	928	222764_at3	**222764_at**	2	2	2	0	0	10	675	223	3	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222764_at&chip_id=3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7331	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7331	Homo sapiens hypothetical protein FLJ22316 (FLJ22316), mRNA /cds=(507,1205) /gb=NM_025080 /gi=13376633 /ug=Hs.7331 /len=1512	Hs.7331	hypothetical protein FLJ22316 FLJ22316

Hs.73793	2	440	929	210512_s_at2	**210512_s_at**	5	2	0	0	0	0	186	587	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=210512_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=73793	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=73793	Homo sapiens vascular endothelial growth factor mRNA, complete cds /cds=(701,1276) /gb=AF022375 /gi=3719220 /ug=Hs.73793 /len=3166	Hs.73793	vascular endothelial growth factor VEGF

Hs.74034	2	441	930	212097_at2	**212097_at**	4	4	3	2	5	0	1124	1864	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212097_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74034	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74034	Homo sapiens caveolin 1, caveolae protein, 22kD (CAV1), mRNA /cds=(278,814) /gb=NM_001753 /gi=15451855 /ug=Hs.74034 /len=2704	Hs.74034	caveolin 1, caveolae protein, 22kD	CAV1

Hs.74131	2	442	931	205894_at2	**205894_at**	4	4	2	1	1	4	774	888	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205894_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74131	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74131	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA /cds=(67,1836) /gb=NM_000047 /gi=4502240 /ug=Hs.74131 /len=1858	Hs.74131	arylsulfatase E (chondrodysplasia punctata 1)	ARSE

Hs.74564	2	443	932	200652_at2	**200652_at**	6	1	0	0	0	1	187	417	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200652_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74564	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=74564	Homo sapiens signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(50,601) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	Hs.74564	signal sequence receptor, beta (translocon-associated protein beta) SSR2

Hs.75249	2	444	933	211935_at2	**211935_at**	7	0	0	0	0	0	106	612	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=211935_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75249	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75249	Homo sapiens, clone MGC:5360 IMAGE:3048642, mRNA, complete cds /cds=(69,680) /gb=BC010281 /gi=16307464 /ug=Hs.75249 /len=2280	Hs.75249	ADP-ribosylation factor-like 6 interacting protein ARL6IP

heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
HSPA5

Hs.75410

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211936_at

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&chip_id=2 410 410 0 /len=3925

d=211936_at =Hs&CID=75 =Hs&CID=75 /ug=Hs.7541

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MGC:31939

clone

sapiens,

Homo

Hs.75410

Hs.75412	2	446	935	202655_at2	**202655_at**	5	3	1	0	0	0	208	592	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202655_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75412	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75412	Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA /cds=(132,836) /gb=NM_006010 /gi=5174392 /ug=Hs.75412 /len=1103	Hs.75412	arginine-rich, mutated in early stage tumors ARMET

Hs.75431	2	447	936	219612_s_at2	**219612_s_at**	7	6	6	6	0	5	299	6	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219612_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75431	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75431	Homo sapiens fibrinogen, gamma polypeptide (FGG), transcript variant gamma-B, mRNA /cds=(42,1403) /gb=NM_021870 /gi=11761632 /ug=Hs.75431 /len=1655	Hs.75431	fibrinogen, gamma polypeptide	FGG

Hs.75655	2	448	937	200654_at2	**200654_at**	5	4	3	1	1	0	435	435	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200654_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75655	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75655	Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA /cds=(29,1555) /gb=NM_000918 /gi=4505566 /ug=Hs.75655 /len=1956	Hs.75655	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	P4HB

Hs.75693	2	449	938	201494_at2	**201494_at**	2	0	0	0	0	2	251	927	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201494_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75693	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75693	Homo sapiens prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA /cds=(29,1519) /gb=NM_005040 /gi=4826939 /ug=Hs.75693 /len=2060	Hs.75693	prolylcarboxypeptidase (angiotensinase C)	PRCP

Hs.75722	2	450	939	208689_s_at2	**208689_s_at**	6	3	1	0	0	0	646	199	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208689_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75722	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75722	Homo sapiens ribophorin II (RPN2), mRNA /cds=(288,2183) /gb=NM_002951 /gi=4506676 /ug=Hs.75722 /len=2509	Hs.75722	ribophorin II RPN2

Hs.75741	2	451	940	203559_s_at2	**203559_s_at**	5	4	3	0	1	5	768	1227	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=203559_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75741	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75741	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), mRNA /cds=(71,2326) /gb=NM_001091 /gi=4501850 /ug=Hs.75741 /len=2407	Hs.75741	amiloride binding protein 1 (amine oxidase (copper-containing)) ABP1

Hs.75761	2	452	941	202200_s_at2	**202200_s_at**	7	3	1	0	0	0	18	329	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202200_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75761	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75761	Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA /cds=(9,1973) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244	Hs.75761	SFRS protein kinase 1 SRPK1

Hs.75790	2	453	942	202846_s_at2	**202846_s_at**	6	1	0	0	0	0	333	745	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202846_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75790	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75790	Homo sapiens phosphatidylinositol glycan, class C (PIGC), mRNA /cds=(293,1186) /gb=NM_002642 /gi=4505794 /ug=Hs.75790 /len=1458	Hs.75790	phosphatidylinositol glycan, class C	PIGC

Hs.75794	2	454	943	204037_at2	**204037_at**	4	2	2	0	1	0	570	429	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204037_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75794	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75794	Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(393,1487) /gb=NM_057159 /gi=16950637 /ug=Hs.75794 /len=2732	Hs.75794	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 EDG2

Hs.7594	2	455	944	202499_s_at2	**202499_s_at**	6	5	5	2	2	0	655	115	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202499_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7594	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7594	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3), mRNA /cds=(242,1732) /gb=NM_006931 /gi=5902089 /ug=Hs.7594 /len=3915	Hs.7594	solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3

Hs.75990	2	456	945	206697_s_at2	**206697_s_at**	4	4	3	2	0	8	574	428	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=206697_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75990	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=75990

Homo sapiens cDNA FLJ31310 fis, clone LIVER1000165, highly similar to HAPTOGLOBIN-1 PRECURSOR /cds=UNKNOWN /gb=AK055872 /gi=16550707 /ug=Hs.75990 /len=3024	Hs.75990	haptoglobin	HP

Hs.76095	2	457	946	201631_s_at2	**201631_s_at**	4	4	2	1	3	0	783	1072	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201631_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76095	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76095	Homo sapiens immediate early response 3 (IER3), transcript variant long, mRNA /cds=(29,610) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345	Hs.76095	immediate early response 3	IER3

Hs.7645	2	458	947	204988_at2	**204988_at**	7	7	7	7	0	5	140	2	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204988_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7645	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=7645	Homo sapiens fibrinogen, B beta polypeptide (FGB), mRNA /cds=(8,1483) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918	Hs.7645	fibrinogen, B beta polypeptide FGB

Hs.76473	2	459	948	201393_s_at2	**201393_s_at**	4	1	1	0	0	1	291	533	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201393_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76473	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76473	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA /cds=(147,7622) /gb=NM_000876 /gi=4504610 /ug=Hs.76473 /len=9090	Hs.76473	insulin-like growth factor 2 receptor IGF2R

Hs.76918	2	460	949	202679_at2	**202679_at**	6	4	2	0	0	0	196	334	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202679_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76918	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=76918	Homo sapiens Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(123,3959) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673	Hs.76918	Niemann-Pick disease, type C1	NPC1

Hs.78183

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1 &chip_id=2 183 183 3 /len=972

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dehydrogena

se, type II)

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member C3

reductase

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Hs.78183

aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)

AKR1C3

Hs.78305	2	462	951	208734_x_at2	**208734_x_at**	4	4	3	0	0	0	554	494	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208734_x_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78305	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=78305	Homo sapiens RAB2, member RAS oncogene family (RAB2), mRNA /cds=(208,846) /gb=NM_002865 /gi=4506364 /ug=Hs.78305 /len=1148	Hs.78305	RAB2, member RAS oncogene family	RAB2
Hs.79069	2	463	952	202769_at2	**202769_at**	6	3	2	0	0	0	218	454	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202769_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79069	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79069	Homo sapiens cyclin G2 (CCNG2), mRNA /cds=(135,1169) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	Hs.79069	cyclin G2	CCNG2

Hs.79217	2	464	953	202148_s_at2	**202148_s_at**	3	0	0	0	0	9	304	896	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202148_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79217	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79217	Homo sapiens pyrroline-5-carboxylate reductase 1 (PYCR1), nuclear gene encoding mitochondrial protein, mRNA /cds=(11,970) /gb=NM_006907 /gi=5902035 /ug=Hs.79217 /len=1792	Hs.79217	pyrroline-5-carboxylate reductase 1	PYCR1

Hs.79339	2	465	954	200923_at2	**200923_at**	8	5	2	1	1	1	503	336	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200923_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79339	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79339	Homo sapiens lectin, galactoside-binding, soluble, 3 binding protein (LGALS3BP), mRNA /cds=(179,1936) /gb=NM_005567 /gi=6006016 /ug=Hs.79339 /len=2254	Hs.79339	lectin, galactoside-binding, soluble, 3 binding protein	LGALS3BP

Hs.79428	2	466	955	201849_at2	**201849_at**	4	4	2	0	0	0	184	546	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201849_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79428	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=79428	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA /cds=(126,710) /gb=NM_004052 /gi=7669480 /ug=Hs.79428 /len=1535	Hs.79428	BCL2/adenovirus E1B 19kD interacting protein 3	BNIP3

Hs.80120	2	467	956	201724_s_at2	**201724_s_at**	4	2	2	0	0	0	320	545	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201724_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80120	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80120	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(31,1710) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1

Hs.80988
2
468
957
201438_at2
201438_at
8 7 6 3 0 0 417 73 2 1 1

Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 1, mRNA /cds=(255,97

http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_info.pl?probeset_id=201438_at&chip_id=2 988

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80988 988

http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=80988 988

bi.nlm.nih.gov/gb=NM_004369

v/UniGene/cl

85)

collagen, type VI, alpha 3

COL6A3

Hs.80988

8 /len=10558

Hs.81086	2	469	958	205421_at2	**205421_at**	4	4	3	2	1	5	583	179	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205421_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81086	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81086	Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA /cds=(27,1697) /gb=NM_021977 /gi=11415037 /ug=Hs.81086 /len=3213	Hs.81086	solute carrier family 22 (extraneuronal monoamine transporter), member 3	SLC22A3

Hs.81665	2	470	959	205051_s_at2	**205051_s_at**	6	4	2	0	3	0	626	144	2	1	1		1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205051_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81665	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=81665	Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA /cds=(21,2951) /gb=NM_000222 /gi=4557694 /ug=Hs.81665 /len=5084	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	KIT

Hs.82292	2	471	960	204866_at2	**204866_at**	5	2	1	0	0	0	209	646	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204866_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82292	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82292	Homo sapiens KIAA0215 gene product (KIAA0215), mRNA /cds=(298,2769) /gb=NM_014735 /gi=7662005 /ug=Hs.82292 /len=4935	Hs.82292	KIAA0215 gene product	KIAA0215

Hs.823	2	472	961	204934_s_at2	**204934_s_at**	1	0	0	0	0	11	135	1050	2	1	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204934_s_at&chip_id=2 3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82 3	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82 3	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), mRNA /cds=(245,1498) /gb=NM_002151 /gi=4504480 /ug=Hs.823 /len=1783	Hs.823	hepsin (transmembrane protease, serine 1)	HPN

Hs.82689	2	473	962	200599_s_at2	**200599_s_at**	5	2	0	0	0	0	266	466	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=200599_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82689	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=82689	Homo sapiens tumor rejection antigen (gp96) 1 (TRA1), mRNA /cds=(105,2516) /gb=NM_003299 /gi=4507676 /ug=Hs.82689 /len=2780	Hs.82689	tumor rejection antigen (gp96) 1	TRA1

Hs.83354	2	474	963	202998_s_at2	**202998_s_at**	8	6	4	0	0	0	117	117	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202998_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83354	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=83354	Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA /cds=(247,2571) /gb=NM_002318 /gi=4505010 /ug=Hs.83354 /len=3432	Hs.83354	lysyl oxidase-like 2 LOXL2

Hs.86347	2	475	964	219293_s_at2	**219293_s_at**	4	0	0	0	0	0	256	862	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219293_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=86347	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=86347	Homo sapiens hypothetical protein (PTD004), mRNA /cds=(116,1306) /gb=NM_013341 /gi=9558756 /ug=Hs.86347 /len=1759	Hs.86347	hypothetical protein PTD004 PTD004
Hs.8858	2	476	965	217986_s_at2	**217986_s_at**	5	5	2	0	1	0	520	799	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=217986_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8858	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8858	Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), mRNA /cds=(115,5139) /gb=NM_013448 /gi=7304918 /ug=Hs.8858 /len=5925	Hs.8858	bromodomain adjacent to zinc finger domain, 1A BAZ1A

Hs.9003	2	477	966	222190_s_at2	**222190_s_at**	1	0	0	0	0	11	585	392	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=222190_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9003	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9003	Homo sapiens hypothetical protein FLJ13868 (FLJ13868), mRNA /cds=(12,1418) /gb=NM_022744 /gi=12232402 /ug=Hs.9003 /len=2760

Hs.9003

hypothetical protein FLJ13868

FLJ13868

granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
GZMA

Hs.90708	2	478	967	205488_at2	**205488_at**	6	4	4	1	0	3	517	649	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=205488_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90708	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90708	Homo sapiens granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA), mRNA /cds=(38,826) /gb=NM_006144 /gi=6996012 /ug=Hs.90708 /len=878	Hs.90708

Hs.90786	2	479	968	208161_s_at2	**208161_s_at**	6	5	5	2	2	0	375	229	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=208161_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90786	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=90786	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA /cds=(70,1602) /gb=NM_020038 /gi=9955973 /ug=Hs.90786 /len=5380	Hs.90786	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	ABCC3

Hs.91165	2	480	969	219694_at2	**219694_at**	5	4	4	0	0	1	421	183	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219694_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=91165	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=91165	Homo sapiens hypothetical protein (FLJ11127), mRNA /cds=(72,1142) /gb=NM_019018 /gi=9506640 /ug=Hs.91165 /len=1925	Hs.91165	hypothetical protein FLJ11127	FLJ11127
Hs.9234	2	481	970	202475_at2	**202475_at**	4	1	0	0	0	0	346	401	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=202475_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9234	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9234	Homo sapiens seven transmembrane domain protein (NIFIE14), mRNA /cds=(106,780) /gb=NM_032635 /gi=14249165 /ug=Hs.9234 /len=878	Hs.9234	seven transmembrane domain protein	NIFIE14

Hs.9235	2	482	971	212739_s_at2	**212739_s_at**	7	6	4	2	0	2	64	131	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212739_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9235	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9235	Homo sapiens non-metastatic cells 4, protein expressed in (NME4), mRNA /cds=(11,574) /gb=NM_005009 /gi=4826861 /ug=Hs.9235 /len=879	Hs.9235	non-metastatic cells 4, protein expressed in NME4

Hs.9265	2	483	972	218270_at2	**218270_at**	4	2	1	0	0	7	265	316	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=218270_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9265	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9265	Homo sapiens hypothetical protein FLJ20917 (FLJ20917), mRNA /cds=(137,787) /gb=NM_024540 /gi=13375698 /ug=Hs.9265 /len=951	Hs.9265	mitochondrial ribosomal protein L24	MRPL24

Hs.94382	2	484	973	204120_s_at2	**204120_s_at**	6	4	0	0	0	0	253	388	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=204120_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=94382	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=94382	Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA /cds=(183,1271) /gb=NM_006721 /gi=5921989 /ug=Hs.94382 /len=1860	Hs.94382	adenosine kinase	ADK

Hs.95655	2	485	974	213716_s_at2	**213716_s_at**	4	4	1	1	1	4	781	953	2	1	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=213716_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=95655	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=95655	Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA /cds=(118,864) /gb=NM_003004 /gi=4506868 /ug=Hs.95655 /len=2000	Hs.95655	secreted and transmembrane 1	SECTM1

Hs.9613	2	486	975	221009_s_at2	**221009_s_at**	5	4	3	1	0	7	540	615	2	1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=221009_s_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9613	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=9613	Homo sapiens angiopoietin-like 4 (ANGPTL4), mRNA /cds=(153,1370) /gb=NM_016109 /gi=7705828 /ug=Hs.9613 /len=1860	Hs.9613	angiopoietin-like 4 ANGPTL4

both scc ad
119 199 176

Hs.96593	2	487	976	219045_at2	**219045_at**	6	4	4	1	0	1	466	624	2		1		1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=219045_at&chip_id=2	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=96593	http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=96593	Homo sapiens ras homolog gene family, member F (in filopodia) (ARHF), mRNA /cds=(21,656) /gb=NM_019034 /gi=9506666 /ug=Hs.96593 /len=2421	Hs.96593	ras homolog gene family, member F (in filopodia)	ARHF
	2	488	977	209744_x_at2	**212460_at**	11	9	6	3	0	0	186	69	2	1			1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=212460_at&chip_id=2						uk5
	2	489	978	213535_s_at2	**201114_x_at**	6	2	2	0	0	5	455	292	2			1	1	http://intranet.metagen.de/cgi-bin/eike/probeset_anno/probeset_anno.pl?probeset_id=201114_x_at&chip_id=2						

Aliases	LLID	UGRepAcc	LLRepProtAcc	Chromosome	Cytoband	SumFunc	GO	ExtAnnot	SPFunction	SPLocal
||ELOVL4||ADMD||STGD2||STGD3||Stargardt disease 3 (autosomal dominant)||ELONGATION OF VERY LONG CHAIN FATTY ACIDS-LIKE 4||elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4||	6785	NM_022726	NP_073563							

||LOC51299|| neuritin||NRN ||	51299	NM_016588	NP_057672	Very strongly similar to rat neuritin; may induce neurite outgrowth and arborization
||hypothetical protein FLJ10702||	55207	NM_018184	NP_060654	Member of the ADP-ribosylation factor (ARF) family; putative GTP-binding protein involved in protein trafficking
||CNTNAP2|| KIAA0868||contactin-associated protein 2||contactin associated protein-like 2||cell recognition molecule Caspr2||homolog of Drosophila neurexin IV||	26047	NM_014141	NP_054860	
||hypothetical protein DKFZp586C1924||	84233	NM_032273	NP_115649	
				may be involved in melanosomal transport and docking.
||RAB38||ANTIGEN NY-MEL-1||Rab-related GTP-binding protein||RAS-RELATED PROTEIN RAB-38||RAS FAMILY, MEMBER RAB38||RAB38, member RAS oncogene family||	23682	NM_022337	NP_071732	

||SKALP||ESI||PI3||ELAFIN PRECURSOR||ANTILEUKOPROTEINASE, SKIN-DERIVED||ELASTASE-SPECIFIC INHIBITOR||SKIN-DERIVED ANTILEUKOPROTEINASE||PROTEINASE INHIBITOR 3||protease inhibitor 3, skin-derived (SKALP)||	5266	NM_002638	NP_002629	Elafin; protease inhibitor that inhibits leukocyte elastase and may be cross-linked to other proteins in the extracellular matrix of the skin	molecular function|protein binding|E|GO:0005515|Proteome|7685029//cellular component|extracellular matrix|E|GO:0005578|Proteome|8476637//molecular function|proteinase inhibitor|E|GO:0004866|Proteome|2394696//molecular function|serine protease inhibitor|P|GO:0004867|Proteome|8476637	biochemical function|Inhibitor or repressor|NR|Proteome|2394696//organismal role|Extracellular matrix maintenance|NR|Proteome|7685029//organismal role|Epidermal Development and Maintenance|NR|Proteome|7685029//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|7685029	neutrophil and pancreatic elastase-specific inhibitor of skin. it may prevent elastase-mediated tissue proteolysis.	secreted.

catalyzes the conversion of leukotriene b4 into its biologically less active metabolite, 12-oxo-leukotriene b4. this is an initial and key step of metabolic inactivation of leukotriene b4 in various tissues other than leukocytes. cytoplasmic.

BM466998

||DRG1||DRG ||NEDD3||DR G 1||developme ntally regulated GTP-binding protein 1||neural precursor cell expressed, development ally down-regulated 3||NEURAL PRECURSO R CELL EXPRESSED . DEVELOPM ENTALLY DOWNREG ULATED 3||	4733	NM_004147	NP_004138	Very strongly similar to murine Drg1; binds the transcription factor SCL, may bind GTP	biological process|trans cription|P|GO :0006350|Pro teome|98246 80//biological process|deve lopmental processes|P| GO:0007275| Proteome|12 80421//molec ular function|trans cription factor binding|E|GO :0008134|Pro teome|98246 80	may play a role in cell proliferation, differentiation and death.	cytoplasmic.

component|membrane fraction|PI|GO:0005624|Proteome|94651 14//molecular function|chol esterol binding|PI|GO:0015485|Proteome|96345 33//molecular function|electron transporter|PI|GO:0005489|Proteome|94 65114//cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|987 8250//biological process|chol esterol metabolism|E|GO:0008203|Proteome|96 65114	||DHCR7||SLOS||STEROL DELTA-7-REDUCTASE||7-@DEHYDROCHOLESTEROL REDUCTASE||Delta-7-dehydrocholesterol reductase||	1717	NM_001360	NP_001351	7-dehydrocholesterol reductase; removes the C7-8 double bond in 7-dehydrocholesterol	biochemical function|Oxidoreductase|E|Proteome|96 34533//subcellular localization|Unspecified membrane|E|Proteome|94 65114

||PCDH-BETA5||PCDH-BETA-5||PCDHB5||DKFZP586B0217||PROTOCADHERIN-BETA 5||protocadherin beta 5 precursor||	Highly similar to rat Rn.10166 protocadherin 3; may act as a receptor or cell adhesion protein; contains cadherin domains	26167	NM_015669	NP_056484	potential calcium-dependent cell-adhesion protein. type i membrane protein (by similarity).

||APMCF1 protein||signal recognition particle receptor, beta subunit||	58477	NM_021203	NP_067026			
||LETM1||LEUCINE ZIPPER/EF-HAND-CONTAINING TRANSMEMBRANE PROTEIN 1||leucine zipper-EF-hand containing transmembrane protein 1||	3954	NM_012318	NP_036450	Leucine zipper transmembrane protein 1; may bind calcium; member of the EF-hand family of calcium-binding proteins	molecular function|calcium binding|P|GO:0005509|Proteome|10486213//biological process|signal transduction|P|GO:0007165|Proteome|10486213//biological process|developmental processes|P|GO:0007275|Proteome|10486213//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|10486213	molecular localization|Integral membrane|NR|Proteome|10486213//subcellular localization|Unspecified membrane|NR|Proteome|10486213

||KIAA0794 protein||	26043	AB018337									
		AK055618	||GHBP||GHR ||GH RECEPTOR|| SERUM BINDING PROTEIN||GROWTH HORMONE RECEPTOR PRECURSOR||GHR GROWTH HORMONE-BINDING PROTEIN||	2690	NM_000163	NP_000154	Growth hormone receptor	biological process|growth pattern|E|GO:0007150|Proteome|9140387//biological process|skeletal development|E|GO:0001501|Proteome|9140387//molecular function|growth hormone receptor|P|GO:0004903|Proteome|9140387//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|2825030	organismal role|Control of body size|NR|Proteome|9140387//biochemical function|Receptor (signalling)|NR|Proteome|9140387//organismal role|Control of Cell Proliferation|NR|Proteome|9341147//organismal role|Bone Development and Maintenance|NR|Proteome|9140387	this is a receptor for pituitary gland growth hormone.	type i membrane protein.

||PARL||hypothetical protein PRO2207||presenilins associated rhomboid-like protein||	55486	NM_018622	NP_061092					
||COX5B||EC 1.9.3.1||cytochrome c oxidase subunit Vb||CYTOCHROME c OXIDASE, SUBUNIT Vb||CYTOCHROME C OXIDASE POLYPEPTIDE VB, MITOCHONDRIAL PRECURSOR||	1329	NM_001862	NP_001853	Subunit Vb of cytochrome c oxidase	biological process|respiration|P|GO:0007585|Proteome|1646156//molecular function|cytochrome-c oxidase|P|GO:0004129|Proteome|1646156	cellular role|Energy generation|P|Proteome|1646156//organismal role|General cellular role|NR|Proteome|1646156//subcellular localization|Mitochondrial|NR|Proteome|na	this protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.	mitochondrial inner membrane.

||P51||KET||S HFM4||p63||P 73H||EEC3||T P63||TUMOR PROTEIN p63||p53-RELATED PROTEIN p63||tumor protein 63 kDa with strong homology to p53||	8626	NM_003722	NP_003713	Similar to p53 (TP53); induces growth-suppression and apoptosis in p53-deficient cells	biological process|induction of apoptosis|E|GO:0006917|Proteome|96 62378	organismal role|Cell death/Apoptosis|E|Proteome|9662378||biochemical function|inhibitor or repressor|E|Proteome|966 2378
||SNX5||sorting nexin 5||	27131	NM_014426	NP_055241	Member of the sorting nexin family; may be involved in receptor trafficking between organelles	biological process|non-selective vesicle transport|P|GO:0006899|Proteome|106 00472	

||HC7-I||PSMB2||EC 3.4.25.1||MACROPAIN SUBUNIT C7-I||PROTEASOME COMPONENT C7-I||PROTEASOME SUBUNIT, BETA-TYPE, 2||MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I||Proteasome subunit, beta type, 2||PROTEASOME SUBUNIT BETA TYPE 2||proteasome (prosome, macropain) subunit, beta type, 2||	5690	NM_002794	NP_002785	Beta subunit 2 of the proteasome (prosome macropain)	cellular component|26S proteasome|P|GO:0005837|Proteome|8811196	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|7918633	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity. this subunit has a chymotrypsin-like activity.	cytoplasmic and nuclear.

Caveolin 2; component of caveolar membranes, may be involved in signal transduction, endocytosis and potocytosis	||CAV2||CAV|| CAVEOLIN-2||caveolae protein, 20-kD||caveolin 2, beta isoform||caveolin 2, alpha isoform||	858	NM_001233	NP_001224	molecular function|tumor suppressor|PI| GO:0008181| Proteome|98 01158	may act as a scaffolding protein within caveolar membranes. interacts directly with g-protein alpha subunits and can functionally regulate their activity. caveolin-2 may function as an accessory protein in conjunction with caveolin-1.	membrane protein of caveolae. potential hairpin-like structure in the membrane (by similarity).		

||GOLPH4||GPP130||GIMPC||golgi phosphoprotein 4||type II Golgi membrane protein||	27333	NM_014498	NP_055313	Golgi membrane phosphoprotein in type II; localizes to the early Golgi, but undergoes modification in the late Golgi and may cycle between the two compartments; contains many predicted coiled-coil domains	cellular component|Golgi lumen|P|GO:0005796|Proteome|9201717//cellular component|Golgi cis-face|E|GO:0005801|Proteome|9201717//cellular component|integral membrane protein|P|GO:0016021|Proteome|9201717//cellular component|endocytotic transport vesicle|E|GO:0005810|Proteome|9201717	subcellular localization|Golgi|NR|Proteome|9201717//molecular localization|Integral membrane|P|Proteome|9201717
||HUF2||TTF2||lodestar protein||transcription termination factor, RNA polymerase II||	8458	NM_003594	NP_003585	ATP-dependent RNA polymerase II transcription termination factor; exhibits ATPase activity which requires double-stranded DNA	biological process|transcription termination|E|GO:0006353|Proteome|9748214//molecular function|DNA dependent adenosinetriphosphatase|E|GO:0008094|Proteome|9748214//cellular component|transcription elongation factor complex|E|GO:0008023|Proteome|9748214//molecular function|Pol II transcription termination factor|E|GO:0003717|Proteome|9748214	biochemical function|Hydrolase|NR|Proteome|9748214//cellular role|Pol II transcription|NR|Proteome|9748214//molecular localization|DNA-associated (direct or indirect)|NR|Proteome|9748214

function|ligan d|P|GO:0005 102|Proteom e|8288227//bi ological process|onco genesis|P|G O:0007048|P roteome|104 91302//cellul ar component|s oluble fraction|P|GO :0005625|Pro teome|10491 302//biologic al process|sign al transduction| ||WNT5A||ON COGENE WNT5A||WN T-5A PROTEIN PRECURSO R||wingless-type MMTV integration site family, member 5A||	Member of the Wnt family of cell signalling proteins; Induces axis duplication in oocytes when coexpressed with hFz5	7474	NM_003392	NP_003383	organismal role|Angiogen esis|P|Proteo me|10491302 //molecular localization|S oluble|P|Prot eome|104913 02//organism al role|Cell-to-cell signaling|NR| P|GO:000716 5|Proteome|1 0491302//cell ular component|e xtracellular xtracellular space|P|GO: 0005615|Prot eome|104913 02//molecular	ligand for members of the frizzled family of seven transmembra ne receptors. probable develop ment al protein. may be a signaling molecule which affects the development of discrete regions of tissues. is likely to signal over only few cell diameters.	possibly secreted and associates with the extracellular matrix.

subcellular localization|Nuclear|E|Prot eome|139419 2//molecular localization|RNA-								
||NOP120||p120||NOL1||PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120||nucleolar protein 1 (120kD)||PROLIFERATING CELL NUCLEOLAR PROTEIN P120||	4839	NM_006170	NP_006161	Nucleolar protein 1; proliferation-associated antigen, transforms NIH3T3 cells when overexpressed	cellular component|Nucleolus|P|GO:0005730|Proteome|13941 92//biological process|cell cycle control|P|GO:0000074|Proteome|139419 2//biological process|positive control of cell proliferation| 394192	associated|P|Proteome|13941 92//biochemical function|RNA-binding protein|P|Proteome|139419 2//cellular role|RNA processing|P|Proteome|13941 92//subcellular localization|Nucleolar proliferation| 4192	may play a role in the regulation of the cell cycle and the increased nucleolar activity that is associated with the cell proliferation.	nuclear; nucleolar.

|NOT56L||CDGS4||CDGId||DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYLMANNOSYLTRANSFERASE||EC 2.4.1.-||DOL-P-MANDEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE||Not56 (D. melanogaster)-like protein||CDGS, TYPE IV NOT56-LIKE PROTEIN||ALG3, S. CEREVISIAE, HOMOLOGOF||CARBOHYDRATE-DEFICIENT GLYCOPRO	10195	NM_005787 NP_005778	Low similarity to S. cerevisiae Rhk1p	adds the first dol-p-man derived mannose in an alpha 1,3 linkage to man5glcnac2-pp-dol. . integral membrane protein. endoplasmic reticulum (probable).

1739	NM_004087	NP_004078	||SAP97||hdlg ||DLG1||PRE SYNAPTIC PROTEIN SAP97||SYN APSE-ASSOCIATE D PROTEIN 97||DISCS, LARGE HOMOLOG 1||discs, large (Drosophila) homolog 1||DISCS LARGE, DROSOPHIL A, HOMOLOG OF, 1||	Homolog of Drosophila discs large tumor suppressor 1; putative kinase, binds EPB41, may have structural and signaling roles; member of the membrane-associated guanylate kinase (MAGUK) family	859302//molecular function|Cellular component|plasma membrane|E|GO:0005886|Proteome|10 59302//cellular component|Proteome|108 roteome|108 859302//biochemical function|Transferase|P|Proteome|88256 52//biochemical function|Other kinase|P|Protein kinase|882565 2//subcellular localization|C ytoplasmic|E|Proteome|10 859302//subcellular localization|C ell junction|P|Proteome|8825 652//organismal role|Cell-to-cell signalling|NR| junction|E|GO:0005911|P roteome|793	interacts with the cytoplasmic tail of nmda receptor subunits. associates with protein 4.1.

||MCM4||CDC54||P1-CDC21||CDC21||CDC21 HOMOLOG||CDC21, S. POMBE, HOMOLOG OF||DNA REPLICATION LICENSING FACTOR MCM4||minichromosome maintenance deficient (S. cerevisiae) 4||MINICHROMOSOME MAINTENANCE, S. CEREVISIAE, HOMOLOG OF, 4||CELL DIVISION CYCLE 21, S. POMBE, HOMOLOG OF||	4173	X74794	Similar to S. cerevisiae CDC54; member of the MCM family of chromatin-binding proteins	cellular component|nucleus|E|GO:0005634|Proteome|7601140//cellular component|chromatin|E|GO:0005717|Proteome|8798650//molecular function|DNA binding|E|GO:0003677|Proteome|8798650//biological process|DNA replication|P|GO:0006260|Proteome|7601140//molecular function|adenosinetriphosphatase|P|GO:0004002|Proteome|7601140	cellular role|DNA synthesis|P|Proteome|7601140//biochemical function|Hydrolase|P|Proteome|7601140//subcellular localization|Nuclear|E|Proteome|7601140//biochemical function|DNA-binding protein|E|Proteome|8798650//molecular localization|DNA-associated (direct or indirect)|E|Proteome|8798650	involved in the control of dna replication.	nuclear (by similarity).

||CBR3||EC 1.1.1.184||CARBONYL REDUCTASE [NADPH] 3||carbonyl reductase (NADPH) 3||NADPH-DEPENDENT CARBONYL REDUCTASE 3||	874	NM_001236	NP_001227	Carbonyl reductase 3; reduces carbonyl compounds to their corresponding alcohols	cellular component|cytosol|NR|GO:0005829|Proteome|na//molecular function|carbonyl reductase (NADPH)|P|GO:0004090|Proteome|9740676	biochemical function|Oxidoreductase|P|Proteome|9740676//subcellular localization|Cytoplasmic|P|Proteome|7705364	cytoplasmic (potential).

||CDHF8||HFAT2||MEGF1||FAT2||protocadherin FAT2||cadherin family member 8||FAT tumor suppressor 2 precursor||FAT tumor suppressor (Drosophila) homolog 2||multiple epidermal growth factor-like domains 1||FAT TUMOR SUPPRESSOR, DROSOPHILA, HOMOLOG OF, 2||	2196	NM_001447	NP_001438	Contains EGF-like domains and an extracellular laminin G domain			
||NY-REN-60||ubiquitin specific protease||	84669	NM_032582	NP_115971				
||MMP11||SL-3||STMY3||ST3||MMP-11||STROMELYSIN-3 PRECURSOR||STROMELYSIN III||MATRIX METALLOPROTEINASE-11||EC 3.4.24.-||matrix metalloproteinase 11 preproprotein||matrix metalloproteinase 11 (stromelysin 3)||	4320	NM_005940	NP_005931	Stromelysin 3; matrix metalloprotease that degrades the extracellular matrix	process|oncogenesis|P|GO:0007048|Proteome|1701851//molecular function|stromelysin 3|E|GO:0004249|Proteome|7746327//cellular component|extracellular matrix|P|GO:0005578|Proteome|1701851//biological process|developmental processes|P|GO:0007275|Proteome|7746327//biological process|proteolysis and peptidolysis|P|GO:0006508|Proteome|1701851//biolog	cellular role|Protein degradation|NR|Proteome|1701851//organismal role|Cell migration/motility|NR|Proteome|7746327//organismal role|Extracellular matrix maintenance|NR|Proteome|1701851//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|1701851	may play an important role in the progression of epithelial malignancies.

||EBDCT||EBD1||COL7A1||EBR1||LONG-CHAIN COLLAGEN||LC COLLAGEN||Collagen VII, alpha-1 polypeptide||COLLAGEN, TYPE VII, ALPHA-1||COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR||collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)||	1294	NM_000094	NP_000085	Alpha 1 subunit of type VII collagen; may link collagen fibrils to the basement membrane; member of a subfamily of collagen extracellular matrix proteins	molecular function|collagen|E|GO:0005202|Proteome|9375848//cellular component|basement membrane|E|GO:0005604|Proteome|9375848//cellular component|collagen type VII|E|GO:0005590|Proteome|9375848//biological process|epidermal differentiation|P|GO:0008544|Proteome|8170945	role|Extracellular matrix component|NR|Proteome|9375848//organismal role|Epidermal Development and Maintenance|NR|Proteome|9375848//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|9375848//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|9375848//subcellular localization|Basement	stratified squamous epithelial basement membrane protein that form anchoring fibrils which may contribute to epithelial basement membrane organization and adherence by interacting with extracellular matrix (ecm) proteins such as type iv collagen.
||DECTIN1||CLECSF12||putative transmembrane protein dectin-1||dendritic cell-associated C-type lectin-1 beta||LECTIN, C-TYPE, SUPERFAMILY MEMBER 12||C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12||	64581	NM_022570	NP_072092				

||CK2N||CSK 2B||PHOSVIT IN||2.7.1.37|| CK2B||CSNK 2B||CK II||CASEIN KINASE II BETA CHAIN||CAS EIN KINASE II, BETA SUBUNIT||ca sein kinase 2, beta polypeptide||	1460	NM_001320	NP_001311	Beta subunit of casein kinase II; serine/threonine kinase implicated in insulin-mediated cell metabolism and growth	molecular function|casein kinase II|P|GO:0004682|Proteome|1856204//biological process|signal transduction|P|GO:0007165|Proteome|2513884		plays a complex role in regulating the basal catalytic activity of the alpha subunit.
T3||SLC25A6 ||ANT 3||ADP/ATP TRANSLOCASE 3||ADENINE NUCLEOTIDE TRANSLOCATOR 3, Y-CHROMOSOMAL||Adenine nucleotide translocator-3 (Y chromosome)||adenine nucleotide translocator 3 (liver)||ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2||solute carrier family 25 (mitochondrial carrier; adenine nucleotide	293,	BC008737		Liver form of adenine nucleotide translocator (ADP/ATP carrier)	biological process|energy pathways|P|GO:0006091|Proteome|8490661//molecular function|adenine transporter|P|GO:0015207|Proteome|8490661//biological process|small molecule transport|P|GO:0006832|Proteome|8490661	cellular role|Energy generation|NR|Proteome|8490661//biochemical function|Active transporter, secondary|NR|Proteome|2829183	

||FGFBP1||HBP17||heparin-binding growth factor binding protein||	9982	NM_005130	NP_005121	Heparin binding protein, binds to growth factors HBGF-1 and HBGF-2 in a noncovalent, reversible manner and inhibits their biological activities	function|heparin binding|E|GO:0008201|Proteome|1885605//cellular component|extracellular space|E|GO:0005615|Proteome|1885605//biological process|cell-cell signalling|E|GO:0007267|Proteome|1885605//biological process|signal transduction|NR|GO:0007165|Proteome|na//biological process|negative control of cell proliferation|E|GO:000828	molecular localization|Soluble|NR|Proteome|1885605//organismal role|Cell-to-cell signalling|NR|Proteome|1885605//biochemical function|Inhibitor or repressor|NR|Proteome|1885605//subcellular localization|Extracellular (excluding cell wall)|E|Proteome|1885605

||CD44R||MDU2||N||MDU3||MIC4||Pgp1||MC56||CD44||HERMES ANTIGEN||CD44 antigen (homing function)||CD44 antigen (homing function and Indian blood group system)||	960	AJ251595	NP_000601	main cell surface receptor for hyaluronate. adhesion to mucosal high endothelial venule and to types i and vi collagen. probably involved in matrix adhesion, lymphocyte activation type i and lymph membrane node homing. protein.

UT||GLUT1|| GLUCOSE TRANSPORTER 1||GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN|| SOLUTE CARRIER FAMILY 2, MEMBER 1||ERYTHROCYTE/HEPATOMA GLUCOSE TRANSPORTER GLUCOSE TRANSPORT DEFECT, BLOOD-BRAIN BARRIER||solute carrier family 2 (facilitated glucose transporter), member 1||	6513	NM_006516	NP_006507	Glucose transporter; has role in transport of glucose across the blood-brain barrier	cellular component|membrane|P|GO:0016020|Proteome|3028891//biological process|glucose transport|P|GO:0015758|Proteome|9462754//cellular component|membrane fraction|P|GO:0005624|Proteome|9462754//molecular function|glucose transporter|P|GO:0005355|Proteome|9462754 ,	molecular localization|Integral membrane|NR|Proteome|3028891//subcellular localization|Unspecified membrane|P|Proteome|9462754//biochemical function|Major Facilitator Superfamily|P|Proteome|9462754//biochemical function|Active transporter, secondary|NR|Proteome|9462754	facilitative glucose transporter. this isoform may be responsible for constitutive or basal glucose uptake. has a very broad substrate specificity; can transport a wide range of aldoses including both pentoses and hexoses.	integral membrane protein. localizes primarily at the cell surface (by similarity).

HAD||ERAB||								
EC								
1.1.1.35||TYP								
E II HADH||3-								
HYDROXYA								
CYL-COA		cellular						
DEHYDROG		component|c						
ENASE		ytoplasm|E|G						
TYPE		O:0005737|P						
III|AMYLOID		roteome|933						
BETA-		8779//cellular						
BINDING		component|pl						
POLYPEPTI		asma						
DE		membrane|E|						
ERAB||SHOR		GO:0005886|					
T-CHAIN		Proteome|93						
TYPE		38779//biolog						
DEHYDROG		ical						
ENASE/RED		process|lipid						
UCTASE		metabolism|P					binds	
XH98G2||HY		|GO:0006629					intracellular	
DROXYACY		|Proteome|93					amyloid-beta.	
L-CoA		38779//molec	biochemical				by interacting	
DEHYDROG		ular	function|Oxid				with amyloid-	
ENASE,		function|7-	oreductase|P|				beta, it may	
TYPE	Putative	alpha-	Proteome|93				contribute to	
II||hydroxyacy	hydroxysteroi	hydroxysteroi	38779//subce				the neuronal	
l-Coenzyme	d	d	llular				dysfunction	
A	dehydrogena	dehydrogena	localization|C				associated	
dehydrogena	se; binds	se|P|GO:000	ytoplasmic|E|				with	
se, type	amyloid-beta	8709|Proteo	Proteome|93				alzheimer	
	peptide	me|9338779	38779				disease.	
	NP_004484							
	NM_004493							
	3028							

||FZE3||FZD7 ||frizzled 7||frizzled (Drosophila) homolog 7||Frizzled, drosophila, homolog of, 7||	8324	NM_003507	NP_003498	Frizzled-7; enhances beta-catenin mediated signaling; similar to frizzled receptor family, has seven transmembrane domains	process|oncogenesis|P|GO:0007048|Proteome|9707618//cellular component|plasma membrane|E|GO:0005886|Proteome|9707618//cellular component|integral membrane protein|P|GO:0016021|Proteome|9707618//molecular function|frizzled receptor ligand receptor|E|GO:0004928|Proteome|9707618//biological process|frizzled receptor signalling pathway|E|G	organismal role|Other development|P|Proteome|9707618//organismal role|Cell fate specification|P|Proteome|9707618//molecular localization|Integral membrane|P|Proteome|9707618//biochemical function|Receptor (signalling)|E|Proteome|9707618	wnt proteins. most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of gsk-3 kinase, nuclear accumulation of beta-catenin and activation of wnt target genes. a second signaling pathway involving pkc and calcium fluxes has been seen	integral membrane protein.
||CTL1||CHOLINE TRANSPORTER-LIKE PROTEIN 1||	23446	NM_080546	NP_536856					
	92703	NM_138391	NP_612400					

||NNT-PEN||NNT||EC 1.6.1.2||PYRIDINE NUCLEOTIDE TRANSHYDROGENASE||nicotinamide nucleotide transhydrogenase||NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL PRECURSOR||	23530	NM_012343	NP_036475	Nicotinamide nucleotide transhydrogenase; proton pump that transfers a hydride ion between NAD(H) and NADP(H)	process|energy pathways|NR|GO:0006091|Proteome|na//molecular function|electron transporter|NR|GO:0005489|Proteome|na//cellular component|integral membrane protein|NR|GO:0016021|Proteome|na//cellular component|respiratory chain complex|NR|GO:0005746|Proteome|na//molecular function|NAD(P)(+) transhydrogenase (B-specific)|P|G	cellular role|Energy generation|NR|Proteome|9524818//biochemical function|Oxidoreductase|NR|Proteome|9524818//subcellular localization|Mitochondrial|NR|Proteome|9524818//molecular localization|Integral membrane|NR|Proteome|9524818	the transhydrogenation between nadh and nadp is coupled to respiration and atp hydrolysis and functions as a proton pump across the membrane.	outside the mitochondrial inner membrane on the matrix side (potential).

||SEC22A||sec22 homolog||	26984	NM_012430	NP_036562	Strongly similar to rat SEC22; may act in the early stages of the secretory pathway; member of the SEC22 family of vesicle trafficking proteins	molecular function|vesicle transport|P|GO:0005480|Proteome|8621431//biological process|ER to Golgi transport|P|GO:0006888|Proteome|8621431//cellular component|endoplasmic reticulum membrane|P|GO:0005789|Proteome|8621431	
||P5||protein disulfide isomerase-related protein||	10130	NM_005742	NP_005733	Member of the protein disulfide isomerase superfamily; contains two thioredoxin-like domains	biological process|protein folding|P|GO:0006457|Proteome|7590364//molecular function|protein disulfide isomerase|P|GO:0003756|Proteome|7590364	biochemical function|Isomerase|P|Proteome|7590364

||LOC51249|| hypothetical protein||	51249	NM_016486	NP_057570					
||KIAA0118 protein||	23011	NM_014999	NP_055814					
||EXOSTOSIN-1||EXT1||EXT||MULTIPLE OSTEOCHONDROMATOSIS||DIAPHYSEAL ACLASIS||EXOSTOSIN 1||exostoses (multiple) 1||MULTIPLE CARTILAGINOUS EXOSTOSES||MULTIPLE EXOSTOSES PROTEIN 1||EXOSTOSES, MULTIPLE, TYPE I||PUTATIVE TUMOR SUPPRESSOR PROTEIN EXT1||	2131	NM_000127	NP_000118	Type II transmembrane glycoprotein in ER, dimer with EXT2 has glycosyltransferase activity, has role in cell surface heparan sulfate glycosaminoglycan synthesis	component|Golgi apparatus|E|GO:0005794|Proteome|10639137//molecular function|tumor suppressor|P|GO:0008181|Proteome|7550340//biological process|signal transduction|P|GO:0007165|Proteome|10878610//biological process|skeletal development|E|GO:0001501|Proteome|9620772//cellular component|endoplasmic reticulum|E|G	subcellular localization|Golgi|E|Proteome|10639137//biochemical function|Transferase|E|Proteome|10639137//molecular localization|Integral membrane|E|Proteome|9620772//organismal role|Bone Development and Maintenance|E|Proteome|9620772	glycosyltransferase required for the biosynthesis of heparan-sulfate. the ext1/ext2 complex possesses substantially higher glycosyltransferase activity than ext1 or ext2 alone. appears to be a tumor suppressor.	type ii membrane protein. endoplasmic reticulum. the ext1/ext2 complex is localized in the golgi apparatus.

||CRTR||CT1||SLC6A8||SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1||SOLUTE CARRIER FAMILY 6, MEMBER 8||solute carrier family 6 (neurotransmitter transporter, creatine), member 8||	6535	NM_005629	NP_005620	Sodium and chloride-dependent creatine transporter; member of neurotransmitter transporter family	process|muscle contraction|P|GO:0006936|Proteome|8661155//molecular function|creatine transporter|NR|GO:0005308|Proteome|na//biological process|neurotransmitter uptake|NR|GO:0001504|Proteome|na//biological process|small molecule transport|E|GO:0006832|Proteome|7953292//cellular component|integral membrane protein|P|GO:0016021|Proteome|7953292	organismal role|Muscle action|NR|Proteome|8661155//organismal role|Neuronal transmission|NR|Proteome|7953292//biochemical function|Active transporter, secondary|E|Proteome|7953292	required for the uptake of creatine.	integral membrane protein.

||P61-YES||YES1||YES||C-YES||oncogene yes-1||EC 2.7.1.112||ONCOGENE YES1||YAMAGUCHI SARCOMA ONCOGENE||PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES||v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1||Yamaguchi sarcoma viral (v-yes-1) oncogene homolog 1||	7525	NM_005433	NP_005424	Putative protein-tyrosine kinase	biological process|protein modification|P|GO:0006464|Proteome|2436037//molecular function|protein tyrosine kinase|P|GO:0004713|Proteome|2436037	biochemical function|Transferase|P|Proteome|2436037		
	2936	NM_000637	NP_000628	Erythrocytic glutathione reductase	biological process|stress response|E|GO:0006950|Proteome|947404//molecular function|electron transporter|E|GO:0005489|Proteome|947404//molecular function|glutathione reductase (NADPH)|E|GO:0004362|Proteome|947404//biological process|response to pest/pathogen/parasite|P|GO:0009613|Proteome|947404	cellular role|Cell stress|E|Proteome|947404//biochemical function|Oxidoreductase|E|Proteome|947404//cellular role|Amino-acid metabolism|NR|Proteome|2185014//organismal role|Anti-pathogen response|P|Proteome|947404	maintain high levels of reduced glutathione in the cytosol.	mitochondrial and cytoplasmic.

	component|cytoplasm|EIGO:0005737|Proteome|10842192//biological process|cell motility|EIGO: 0006928|Proteome|963021 6//biological process|inflammatory response|NRI GO:0006954| Proteome|na/ 80156//subcellular localization|CytoplasmicIEI Proteome|10842192//organismal biochemical function|Oxidoreductase|EI Proteome|13							
||COX2||PGHS2||COX-2||PTGS2||PGHS-2||EC 1.14.99.1||CYCLOOXYGENASE 2||CYCLOOXYGENASE - 2||PHS II||PGH SYNTHASE 2||PROSTAGLANDIN H2 SYNTHASE 2||PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR||prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)||	5743	NM_000963	NP_000954	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase).	Prostaglandin H synthase, cyclooxygenase 2); regulates angiogenesis and cell migration, catalyzes the rate-limiting step in the formation of inflammatory prostaglandins	may have a role as a major mediator of inflammation and/or a role for prostanoid signaling in activity-dependent plasticity.	membrane-associated. microsomal membrane.

molecular function|hexokinase|E|GO:0004396|Proteome|927843|biological process|cell cycle control|P|GO:0000074|Proteome|927843|biological process|glucose catabolism|NR|GO:00060 07|Proteome|na//biological process|glucose metabolism|NR|GO:00060 06|Proteome|na//cellular component|mitochondrial outer membrane|R|GO:00057 41|Proteome|na	||HXK2||HK2||HKII||hexokinase 2||hexokinase 2, muscle||HK|||EC 2.7.1.1||MUSCLE FORM HEXOKINASE||HEXOKINASE, TYPE II|||	3099	Z46376	NP_000180	Hexokinase II; converts aldo- and keto-hexose sugars to the hexose-6-phosphate	kinase|E|Proteome|927843|subcellular localization|Mitochondrial|Proteome|76 22509	bound to the outer mitochondrial membrane. its hydrophobic n-terminal sequence may be involved in membrane binding (by similarity).

||HELLS||SMARCA6||PASG||LSH||helicase, lymphoid-specific||	3070	AF155827						
||TM||FETOMODULIN||CD141||THRM||THBD||THROMBOMODULIN PRECURSOR||CD141 ANTIGEN||	7056	NM_000361	NP_000352	Thrombomodulin; changes the procoagulant thrombin into an anticoagulant	molecular function|receptor|P|GO:0004872|Proteome|2822087//molecular function|calcium binding|E|GO:0005509|Proteome|10336638//biological process|blood coagulation|E|GO:0007596|Proteome|9252393//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|2822087	organismal role|Blood clotting|E|Proteome|9252393//molecular localization|Integral membrane|NR|Proteome|2822087//biochemical function|Receptor (signalling)|NR|Proteome|2822087	ulin is a specific endothelial cell receptor that forms a 1:1 stoichiometric complex with thrombin. this complex is responsible for the conversion of protein c to the activated protein c (protein ca). once evolved, protein ca scissions the activated cofactors of the coagulation mechanism, factor va and factor viiia, and thereby reduces the	type i membrane protein.

UMPS||OMP DECASE||OPRT||EC 2.4.2.10||EC 4.1.1.23||OROTICACIDURIA ||UMP SYNTHASE DEFICIENCY ||URIDINE 5'-MONOPHOSPHATE SYNTHASE|| OROTIDINE 5'-PHOSPHATE DECARBOXYLASE||URIDINE MONOPHOSPHATE SYNTHASE DEFICIENCY ||OPRT AND OMP DECARBOXYLASE DEFICIENCY ||UMPS DEFICIENCY	7372	NM_000373	NP_000364	Bifunctional uridine monophosphate (UMP) synthetase; orotate phosphoribosyltransferase and orotidine 5'-monophosphate decarboxylase activities; required for de novo pyrimidine biosynthesis	biological process|UMP biosynthesis|GO:0006222|Proteome|6893554||molecular function|orotate phosphoribosyltransferase|GO:0004588|Proteome|6893554||molecular function|orotidine-5'-phosphate decarboxylase|GO:0004590|Proteome|6893554	biochemical function|Transferase|Proteome|68935 54

||SMOC2||secreted modular calcium-binding protein 2||	64094	AJ420521	C18||CD146|| CD146 ANTIGEN||melanoma adhesion molecule||MELANOMA-ASSOCIATED ANTIGEN MUC18||MELANOMA-ASSOCIATED ANTIGEN A32||MELANOMA-ASSOCIATED GLYCOPROTEIN MUC18||S-ENDO 1 ENDOTHELIAL-ASSOCIATED ANTIGEN||melanoma cell adhesion molecule||CELL SURFACE	4162	NM_006500	NP_006491	Melanoma cell adhesion molecule; may be a neural crest cell adhesion molecule during embryogenesis; member of the immunoglobulin superfamily	process|cell adhesion|P|GO:0007155|Proteome|8378324//molecular function|cell adhesion|P|GO:0005194|Proteome|8378324//molecular function|tumor antigen|E|GO:0008222|Proteome|2602381//cellular component|plasma membrane|NR|GO:0005886|Proteome|na//biological process|embryogenesis and morphogenesis|P|GO:0007345|Proteome|8378324//	organismal role|Embryonic development|P|Proteome|8378324//biochemical function|Adhesin/agglutinin|P|Proteome|8378324//molecular localization|Integral membrane|NR|Proteome|2602381	could be an adhesion molecule active in neural crest cells during embryonic development. its expression may allow melanoma cells to interact with cellular elements of the vascular system thereby enhancing hematogeneous tumor spread.	type i membrane protein.

10||SCYB10||IP10||IP-10||INP10||GAMMA-IP10||gamma IP10||INTERFERON-GAMMA-INDUCED FACTOR||INTERFERON-GAMMA-INDUCIBLE PROTEIN 10||INTERFERON-GAMMA INDUCED PROTEIN||interferon-inducible cytokine IP-10||MOB1, MOUSE, HOMOLOG OF||SMALL INDUCIBLE CYTOKINE B10 PRECURSOR||interferon	3627	NM_001565	NP_001556	IFN-gamma-inducible protein; may have chemotactic and mitogenic activity; member of C-X-C chemokine family	function|ligand|P|GO:0005102|Proteome|10201891//molecular function|chemokine|E|GO:0008009|Proteome|10903763//biological process|chemotaxis|E|GO:0006935|Proteome|10903763//biological process|circulation|P|GO:0008015|Proteome|8798675//biological process|cell motility|NR|GO:0006928|Proteome|na//cellular component|extracellular|NR|GO:0005576|Proteome|	molecular localization|Soluble|P|Proteome|10201901//organismal role|Anti-pathogen response|NR|Proteome|3925348//organismal role|Cell migration/motility|E|Proteome|10903763//organismal role|Cell-to-cell signalling|P|Proteome|3925348	chemotactic for monocytes and t lymphocytes. binds to cxcr3.	secreted.

||STMY2||MMP-10||MMP10||TRANSIN-2||SL-2||STROMELYSIN-2 PRECURSOR||STROMELYSIN II||MATRIX METALLOPROTEINASE-10||transin 2||EC 3.4.24.22||matrix metalloproteinase 10 preproprotein ||matrix metalloproteinase 10 (stromelysin 2)||	4319	NM_002425	NP_002416	Stromelysin 2; matrix metalloprotease that degrades connective tissue	molecular function|zinc binding|P|GO:0008270|Proteome|2844164//cellular component|extracellular space|P|GO:0005615|Proteome|2844164//cellular component|extracellular matrix|P|GO:0005578|Proteome|2844164//molecular function|metalloendopeptidase|P|GO:0004222|Proteome|2844164//biological process|proteolysis and peptidolysis|P|GO:0006508|Proteome|2844164	cellular role|Protein degradation|NR|Proteome|2844164//organismal role|Extracellular matrix maintenance|NR|Proteome|2844164//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|2844164	can degrade fibronectin, gelatins of type i, iii, iv, and v; weakly collagens iii, iv, and v. activates procollagenase.

cellular component|integrin|NR|GO:0008305|Proteome|na|molecular function|cell adhesion receptor|NR|GO:0004895|	Alpha 6 subunit of integrin; acts as a laminin receptor, important for the formation of hemidesmosomes of stratified squamous and transitional epithelia	NP_000201	NM_000210	3655	||VLA-6||ITGA6||CD49f||INTEGRIN, ALPHA-6||INTEGRIN ALPHA-6 PRECURSOR||integrin, alpha 6||integrin alpha chain, alpha 6||	Proteome|na/biological process|cell-substrate junction assembly|E|GO:0007044|Proteome|91|85503	biochemical function|Receptor (signalling)|NR|Proteome|9|185503//organismal role|Epidermal Development and Maintenance|Proteome|91|185503	integrin alpha-6/beta-1 is a receptor for laminin on platelets. integrin alpha-6/beta-4 is a receptor for laminin in epithelial cells and it plays a critical structural role in the hemidesmosome.	type i membrane protein.

||D2S87E||RDC1||CMKOR1||GPRN1||chemokine orphan receptor||canine orphan receptor RDC1 homolog||G PROTEIN-COUPLED RECEPTOR RDC1 HOMOLOG||	57007	U67784						
||MASK||MST4||STE20-like kinase MST4||serine/threonine protein kinase MASK||	51765	NM_016542	NP_057626	Contains a eukaryotic serine/threonine protein kinase domain				
||B15||CI-B15||NDUFB4||EC 1.6.99.3||EC 1.6.5.3||COMPLEX I-B15||NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT||NADH-UBIQUINONE OXIDOREDUCTASE 1 BETA SUBCOMPLEX, 4||NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15)||	4710	NM_004547	NP_004538	Subunit of NADH-ubiquinone oxidoreductase (complex I); transports electrons from NADH to ubiquinone	process|energy pathways|NR|GO:0006091|Proteome|na//cellular component|membrane fraction|NR|GO:0005624|Proteome|na//biological process|complex I (NADH to ubiquinone)|P|GO:0006120|Proteome|9878551//cellular component|NADH dehydrogenase (ubiquinone)|P|GO:0005748|Proteome|9878551//molecular function|NADH	cellular role|Energy generation|NR|Proteome|9878551//biochemical function|Oxidoreductase|NR|Proteome|9878551//organismal role|General cellular role|NR|Proteome|9878551//subcellular localization|Mitochondrial|NR|Proteome|9878551//subcellular localization|Unspecified membrane|NR|Proteome|9878551	transfer of electrons from nadh to the respiratory chain. the immediate electron acceptor for the enzyme is believed to be ubiquinone.	mitochondrial inner membrane; matrix side.

||DKFZP586F 1524 protein||	26073	NM_015584	NP_056399	Region moderately similar to C. elegans ZK652.9	
||AMN||amnionless protein||AMNIONLESS, MOUSE, HOMOLOG OF||visceral endoderm-specific type 1 transmembrane protein||	81693	NM_030943	NP_112205		
||HUR7||SERPINB13||PI13||protease inhibitor 13 (hurpin, headpin)||SERINE PROTEASE INHIBITOR, CLADE B, MEMBER 13||serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13||	5275	NM_012397	NP_036529	Serine proteinase inhibitor; member of the ovalbumin serpin family	molecular function|serpin|P|GO:0004868|Proteome|10512713//biological process|UV response|E|GO:0009411|Proteome|9297979 biochemical function|Inhibitor or repressor|NR|Proteome|10512713//organismal role|Epidermal Development and Maintenance|P|Proteome|10512713

||hypothetical protein PRO2577||	55493	NM_018630	NP_061100	||CLCA2||Calcium CC||CHLORIDE CHANNEL, CALCIUM-ACTIVATED, 2||calcium activated chloride channel 2 precursor||chloride channel, calcium activated, family member 2||	9635	NM_006536	NP_006527	Calcium-sensitive chloride channel 2; displays an outward rectifying conductance of anions; contains five transmembrane domains	transport|E|GO:0006832|Proteome|103 62588//cellular component|in tegral plasma membrane protein|P|GO:0005887|Prot eome|103625 88	molecular function|chloride channel|E|GO:0005254|Proteome|103 62588//biological process|small molecule	molecular function|In localization|In tegral membrane|P| Proteome|10 362588//biochemical function|Cha nnel |passive transporter||E |Proteome|10 362588

||TCF19||SC1 ||transcription factor 19 (SC1)||transcription factor like #||	6941	S53374	NP_009040	Putative transcription factor; may be involved in the later stages of cell cycle progression	biological process|cell cycle control|P|GO:0000074|Proteome|1868030//biological process|cell proliferation|P|GO:0008283|Proteome|1868030//molecular function|transcription factor|P|GO:0003700|Proteome|1868030//biological process|transcription regulation from Pol II promoter|P|GO:0006357|Proteome|1868030	organismal role|Control of Cell Proliferation|P|Proteome|1868030	
||BRAK||NJAC||SCYB14||CHEMOKINE BRAK||SMALL INDUCIBLE CYTOKINE B14 PRECURSOR||CXC chemokine in breast and kidney||SMALL INDUCIBLE CYTOKINE SUBFAMILY B, MEMBER 14||small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)||	9547	NM_004887	NP_004878	Cytokine B14; CXC chemokine that regulates leukocyte infiltration into inflamed tissue	function|chemokine|E|GO:0008009|Proteome|10049774//biological process|chemotaxis|E|GO:0006935|Proteome|10049774//biological process|immune response|NR|GO:0006955|Proteome|na//biological process|signal transduction|P|GO:0007165|Proteome|10049774//biological process|cell-cell signalling|P|GO:0007267|Proteome|10049774//biolog	molecular localization|Soluble|NR|Proteome|10049774//organismal role|Response to injury|NR|Proteome|10049774//organismal role|Anti-pathogen response|NR|Proteome|10049774//organismal role|Cell migration/motility|NR|Proteome|10049774//organismal role|Cell-to-cell signalling|NR|Proteome|10049774	not chemotactive for t-cells, b-cells, monocytes, natural killer cells or ghranulocytes. does not inhibit proliferation of myeloid progenitors in colony formation assays.

				the asymmetric unit membrane (aum); a highly specialized biomembrane elaborated by terminally differentiated urothelial cells. may play an important role in normal bladder epithelial physiology, possibly in regulating membrane permeability of superficial umbrella cells or in stabilizing the apical membrane through aum/cytoskel	integral membrane protein.
||CECR5||hypothetical protein FLJ20454||cat eye syndrome chromosome region, candidate 5, isoform 1||	27440	NM_017829	NP_149061	Protein of unknown function	
||LOC56963|| hypothetical protein from EUROIMAGE 363668||	56963	AL136826			
||UPIB||tetraspan||UPK1||UPK1B||UROPLAKIN IB||uroplakin 1B||	7348	BC012851	NP_008883		

||hypothetical protein MGC1346||	84844	NM_032758	NP_116147			
97-MAPK||PRKM6||ERK-3||MAPK6||ERK3||EC 2.7.1.-||MAP kinase isoform p97||PROTEIN KINASE, MITOGEN-ACTIVATED, 6||extracellular signal-regulated kinase 3||mitogen-activated protein kinase 6||protein kinase, mitogen-activated 6 (extracellular signal-regulated kinase, p97)||protein kinase, mitogen-	5597	NM_002748	NP_002739	MAP kinase 6; activated in response to growth factors	biological process|signal transduction|P|GO:0007165|Proteome|2032290//biological process|protein phosphorylation|E|GO:0006468|Proteome|2032290//molecular function|protein serine/threonine kinase|E|GO:0004674|Proteome|2032290	phosphorylates microtubule-associated protein-2 (map2). may promote entry in the cell cycle (by similarity).

||GFM||FLJ13632||EFG||EFG1||FLJ20773||elongation factor G1||hypothetical protein FLJ12662||mitochondrial elongation factor G||	85476	NM_024996	NP_079272					
||AK3||2.7.4.10||GTP:AMP phosphotransferase||Adenylate kinase-3, mitochondrial||adenylate kinase 3||ADENYLATE KINASE, MITOCHONDRIAL||	205	NM_013410	NP_037542	Adenylate kinase 3; strongly similar to murine Ak4	biological process|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|NR|GO:0006139|Proteome|na			
PA||TPA||alteplase||reteplase||t-plasminogen activator||EC 3.4.21.68||TISSUE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR||TPA PLASMINOGEN ACTIVATOR, TISSUE TYPE, INCREASE IN||plasminogen activator, tissue type isoform 1 preproprotein||plasminogen activator, tissue type isoform 3 precursor||plasminogen activator, tissue type	5327	NM_000930	NP_127509	Tissue-type plasminogen activator; serine protease that converts inactive plasminogen to plasmin	biological process|blood coagulation|E|GO:0007596|Proteome|3839198//biological process|protein modification|E|GO:0006464|Proteome|3087818//molecular function|T-plasminogen activator|E|GO:0004296|Proteome|2838384//biological process|proteolysis and peptidolysis|E|GO:0006508|Proteome|3087818	organismal role|Blood clotting|NR|Proteome|3839198//organismal role|Response to injury|NR|Proteome|3087818	converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single arg-val bond in plasminogen. by controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.	secreted; extracellular.

||PPIL1||CGI-124||CYPL1|| CYCLOPHILIN-RELATED GENE 1||PEPTIDYL-PROLYL ISOMERASE-LIKE 1||peptidylprolyl isomerase (cyclophilin)-like 1||	51645	NM_016059	NP_057143	||CT2||SLC6A10||CT-2||CREATINE TRANSPORTER, TESTIS SPECIFIC||SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2||SOLUTE CARRIER FAMILY 6, MEMBER 10||solute carrier family 6 (neurotransmitter transporter, creatine), member 10||	
||EDJ||DNAJB11||HEDJ||ER-associated DNAJ; ER-associated Hsp40 co-chaperone; hDj9; ERj3||DnaJ (Hsp40) homolog, subfamily B, member 11||	51726	NM_016306	NP_057390			

regulates the synthesis of the neurotransmitter acetylcholine in cholinergic nerve terminals by sodium-driven high-affinity uptake of choline. integral membrane protein.

||HLUGP1||UGT1F||GNT1||UGT1A6||UDP-GLYCOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A6||UDP glycosyltransferase 1 family, polypeptide A6||	54578	NM_001072	NP_001063			
GT1||UGT1A||UGT1A5||GNT1||PHENOL/BILIRUBIN UDP-GLUCURONOSYLTRANSFERASE||URIDINE DIPHOSPHATE GLUCURONOSYLTRANSFERASE, BILIRUBIN/PHENOL||UDP-GLYCOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A1||UDP glycosyltransferase 1 family, polypeptide A1||URIDINE DIPHOSPHATE GLYCOSYLTRANSFERASE 1 FAMILY,	54658	NM_000463	NP_000454	UDP-glucuronosyltransferase; forms conjugates of bilirubin IX alpha and alkyl phenols	biological process|digestion|NR|GO:0007586|Proteome|na//biological process|estrogen metabolism|E|GO:0008210|Proteome|8780690//biological process|bilirubin conjugation|E|GO:0006789|Proteome|1339448//molecular function|UDP-glucuronosyltransferase|E|GO:0003981|Proteome|8780690	cellular role|Other metabolism|E|Proteome|1339448//biochemical function|Transferase|E|Proteome|1339448

||AT1||AT-1||ACATN||ACETYL-CoA TRANSPORTER||acetyl-coenzyme A transporter||	9197	NM_004733	NP_004724	Putative acetyl-Coenzyme A transporter; required for the formation of O-acetylated gangliosides	component|membrane fraction|P|GO:0005624|Proteome|9096318//molecular function|acetyl-CoA transporter|P|GO:0008521|Proteome|9096318//biological process|small molecule transport|P|GO:0006832|Proteome|9096318//cellular component|endoplasmic reticulum membrane|E|GO:0005789|Proteome|9096318//cellular component|integral plasma membrane protein|P|GO:	molecular localization|Integral membrane|P|Proteome|9096318//subcellular localization|Unspecified membrane|P|Proteome|9096318	
	5062	NM_002577	NP_002568	Serine/threonine protein kinase; functions as an effector molecule for Rac1 and Cdc42; member of the PAK family of kinases	molecular function|protein kinase|E|GO:0004672|Proteome|10748018//biological process|signal transduction|P|GO:0007165|Proteome|7744004//biological process|protein phosphorylation|E|GO:0006468|Proteome|7744004//biological process|protein kinase inhibition|E|GO:0006469|Proteome|10748018	biochemical function|Transferase|NR|Proteome|7744004	the activated kinase acts on a variety of targets. phosphorylates ribosomal protein s6, histone h4 and myelin basic protein.

||F11R||JAM1 ||PAM-1||JAM||junctional adhesion molecule 1||JUNCTION ADHESION MOLECULE, MOUSE, HOMOLOG OF||junctional adhesion molecule; platelet adhesion molecule PAM-1||	50848	NM_016946	NP_653087	Junctional adhesion molecule; has a role in lymphocyte homing	molecular function|cell adhesion|E|GO:0005194|Proteome|10395639//biological process|cell motility|NR|GO:0006928|Proteome|na//biological process|inflammatory response|P|GO:0006954|Proteome|10395639//cellular component|intercellular junction|E|GO:0005911|Proteome|10395639	biochemical function|Adhesin/agglutinin|E|Proteome|10395639//organismal role|Anti-pathogen response|NR|Proteome|10395639//subcellular localization|Cell junction|NR|Proteome|10395639//organismal role|Cell migration/motility|NR|Proteome|10395639	plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. involved in platelet activation.	type i membrane protein (potential).
||hypothetical protein FLJ23322||	80020	NM_024955	NP_079231					

Very strongly similar to rat Rn.21394 (translocon-associated protein gamma, signal sequence receptor gamma); may have a role in the translocation of newly synthesized polypeptides across the endoplasmic reticulum membrane	cellular component|microsome|EIG O:0005792|PROTEOME|791 6687//molecular function|signal sequence receptor|EIG O:0005048|PROTEOME|791 6687	||TRAPG||SSR3||TRANSLOCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT||signal sequence receptor, gamma (translocon-associated protein gamma)||	6747	NM_007107	NP_009038	||hypothetical protein FLJ13194||	80218	NM_025146	NP_079422

AP||SAP-3||GM2A||HEXOSAMINIDASE ACTIVATOR DEFICIENCY||GM2-GANGLIOSIDOSIS, TYPE AB||TAY-SACHS DISEASE, AB VARIANT||GANGLIOSIDE GM2 ACTIVATOR PRECURSOR||SHINGOLIPID ACTIVATOR PROTEIN 3||cerebroside sulfate activator protein||AB VARIANT GM2-GANGLIOSIDOSIS GM2-	2760	NM_000405	NP_000396	gangliosides and stimulates ganglioside gm2 degradation. it stimulates only the breakdown of ganglioside gm2 and glycolipid ga2 by beta-hexosaminidase a. it extracts single gm2 molecules from membranes and presents them in soluble form to beta-hexosaminidase a for cleavage of n-acetyl-d-galactosamine and conversion to lysosomal.

3371	NM_002160	NP_002151							
||TN-C||TENASCIN-C||NEURONECTIN||HXB||J||TNC||GMEM||TN||MIOTENDINOUSANTIGEN||Hexabrachion (tenascin)||TENASCINPRECURSOR||GP 150-225||GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN||hexabrachion (tenascin C, cytotactin)||	Hexabrachion (tenascin C), an extracellular matrix glycoprotein; has epidermal growth factor-like repeats	biological process|cell adhesion|P|GO:0007155|P roteome|170 4365//cellular componentle xtracellular matrix|NR|GO:0005578|Proteome|na// molecular function|cell adhesion receptor|P|GO:0004895|Proteome|170 4365//molecular extracellular matrix function|ligand binding or carrier|P|GO:0005488|Proteome|170436 5	cellular role|Cellular structure|E|Proteome|1095 3015//organismal role|Extracellular matrix component|E|Proteome|10 953015//subcellular localization|E|Proteome|170436 5//subcellular localization|E|Proteome|170436 xtracellular (excluding cell wall)|NR|Proteome|170436 xtracellular matrix (cuticle and basement membrane)|E|Proteome|10 953015	sam (substrate-adhesion molecule) that appears to inhibit cell migration. may play a role in supporting the growth of epithelial tumors. is a ligand for integrins alpha-8/beta-1, alpha-9/beta-1, alpha-v/beta-3 and alpha-v/beta-6.	extracellular matrix.				

component|cytoplasm|NR|GO:0005737|Proteome|na//molecular function|calcium binding|P|GO:0005509|Proteome|13218|biological process|actin modification|E|GO:000701 3|Proteome|1321812//cellular component|actin cytoskeleton|E|GO:001562 9|Proteome|1321812//molecular function|actin filament severing|E|GO:0003789|Proteome|831 0295//molecular function|actin filament severing|E|GO:0003789|Proteome|831 0295//molecular	||BREVIN||GSN||AGEL||ADF||ACTIN-DEPOLYMERIZING FACTOR||GELSOLIN PRECURSOR, PLASMA||gelsolin (amyloidosis, Finnish type)|||	2934	NM_000177	NP_000168	Gelsolin; calcium-dependent protein, severs and caps actin filaments	cellular role|Cellular structure|NR|Proteome|30 20431//subcellular localization|Cytoskeletal|NR|Proteome|3 020431//biochemical function|Complex assembly protein|NR|Proteome|1321 812//molecular function|actin localization|Actin-binding|P|GO:0051015|Proteome|831 associated|NR|Proteome|3 020431	calcium-regulated, actin-modulating protein that binds to the plus (or barbed) ends of actin monomers or filaments, preventing monomer exchange (end-blocking or capping). it can promote the assembly of monomers into filaments (nucleation) as well as sever filaments already formed.	secreted (plasma form) and cytoplasmic.

||KIAA1382||A TA2||amino acid transporter 2||AMINO ACID TRANSPOR TER A2||	54407	NM_018976	NP_061849									
||DKFZp762K 137||hypothet ical protein FLJ23399||	64778	NM_022763	NP_073600	||ETK2||Hek2| |Tyro6||EphB 3||EC 2.7.1.112||EP H-like tyrosine kinase- 2||ephrin receptor EphB3||TYR OSINE- PROTEIN KINASE RECEPTOR HEK- 2||EPHRIN TYPE-B RECEPTOR 3 PRECURSO R||eph-like tyrosine kinase 2 (human embryo kinase 2)||	2049	NM_004443	NP_004434	Eph-related receptor tyrosine kinase B3	biological process|sign al transduction| P|GO:000716 5|Proteome|8 397371//cellu lar component|in tegral plasma membrane protein|P|GO: 0005887|Prot eome|839737 1//molecular function|trans membrane receptor protein tyrosine kinase|P|GO: 0004714|Prot eome|839737 1	molecular localization|In tegral membrane|N R|Proteome|8 397371//bioc hemical function|Rece ptor (signalling)|N R|Proteome|8 397371	receptor for members of the ephrin-b family. binds to ephrin-b1 and -b2.	type i membrane protein.

			||p53-induced protein PIGPC1||			
64065	NM_022121	NP_071404	||EDG8||S1P RECEPTOR EDG8||ENDOTHELIAL DIFFERENTIATION GENE 8||sphingosine 1-phosphate receptor Edg-8||SPHINGOSINE 1-PHOSPHATE RECEPTOR EDG8||endothelial differentiation, sphingolipid G-protein-coupled receptor, 8||			
53637	NM_030760	NP_110387	||SGN2||TRIP15||COPS2-PENDING||ALIEN||COPS2||COP9, SUBUNIT 2||ALIEN, DROSOPHILA, HOMOLOG OF||THYROID HORMONE RECEPTOR INTERACTOR 15||thyroid receptor interacting protein 15||			
9318	NM_004236	NP_004227		Subunit of the COP9 signalosome complex; involved in signal transduction	molecular function|protein binding|E|GO:0005515|Proteome|9535219//biological process|signal transduction|P|GO:0007165|Proteome|9535219//biological process|transcription from Pol II promoter|P|GO:0006366|Proteome|7776974	cellular role|Pol II transcription|P|Proteome|7776974

||DKFZP434F1735 protein||	26079	NM_015590	NP_056405						
||hypothetical protein FLJ10407||	55706	AL354613	NP_060557						
	1645	NM_001353	NP_001344	ALPHA-HSD||MBAB||20-ALPHA-HSD||H-37||DD1||DD2||HBAB||AKR1C1||HAKRC||DDH||EC 1.3.1.20||20 ALPHA-HYDROXYSTEROID DEHYDROGENASE||ALDO-KETO REDUCTASE C||DIHYDRODIOL DEHYDROGENASE 2||DIHYDRODIOL DEHYDROGENASE, TYPE I||CHLORDECONE REDUCTASE HOMOLOG	Dihydrodiol dehydrogenase (3-alpha-hydroxysteroid dehydrogenase); hepatic bile acid binding protein, metabolizes xenobiotics	function|enzyme|E|GO:0003824|Proteome|8486699//cellular component|cytoplasm|NR|GO:0005737|Proteome|na//molecular function|aldo-keto reductase|P|GO:0004033|Proteome|7789999//biological process|xenobiotic metabolism|P|GO:0006805|Proteome|8486699//molecular function|bile acid transporter|P|GO:0015125|Proteome|8486699//molecular	biochemical function|Oxidoreductase|NR|Proteome|7515059//subcellular localization|Cytoplasmic|NR|Proteome|8486699//biochemical function|Small molecule-binding protein|NR|Proteome|8486699	may assist in the rapid intracellular transport of bile acids from the sinusoidal to the canalicular pole of the cell. have a role in monitoring the intrahepatic bile acid concentration.	cytoplasmic.

AK055663	||SFRP2||FRP-2||SARP1||SDF-5||secreted frizzled-related protein 2||SECRETED APOPTOSIS-RELATED PROTEIN 1||secreted apoptosis related protein 1||							
BC008666	||ETA-1||OPN||SPP-1||NEPHROPONTIN||UROPONTIN||BNSP||BSPI||SPP1||OSTEOPONTIN PRECURSOR||URINARY STONE PROTEIN||BONE SIALOPROTEIN 1||Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)||secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)||	6696	NM_000582	NP_000573	Osteopontin (bone sialoprotein); bone and blood vessel extracellular matrix protein involved in calcification and atherosclerosis	biological process|ossification|E|GO:0001503|Proteome|10766759//cellular component|extracellular matrix|E|GO:0005578|Proteome|10751402//biological process|skeletal development|NR|GO:0001501|Proteome|na	organismal role|Bone Development and Maintenance|E|Proteome|10766759//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|2404984//subcellular localization|Extracellular matrix (cuticle and basement membrane)|E|Proteome|10751402	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.

||hypothetical protein MGC3279 similar to collectins||	78989	NM_024027	NP_076932					
||DFNB1||NSRD1||PPK||DFNA3||CX26||GJB2||GAP JUNCTION PROTEIN, 26-KD||deafness, autosomal recessive 1||GAP JUNCTION PROTEIN, BETA-2||GAP JUNCTION BETA-2 PROTEIN||deafness, autosomal dominant 3||gap junction protein, beta 2, 26kD (connexin 26)||	2706	M86849	NP_003995	Connexin 26; gap junction protein expressed in various tissues including cochlea	process|hearing|E|GO:0007605|Proteome|9482292//cellular component|connexon|P|GO:0005922|Proteome|1324944//cellular component|plasma membrane|E|GO:0005886|Proteome|1324944//molecular function|connexon channel|P|GO:0015285|Proteome|1324944//biological process|cell-cell signalling|P|GO:0007267|Proteome|1324944//biological	subcellular localization|Cell junction|E|Proteome|1324944//organismal role|Intercellular transport|P|Proteome|1324944//molecular localization|Integral membrane|NR|Proteome|1324944//biochemical function|Channel [passive transporter]|P|Proteome|1324944	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	integral membrane protein.

||hypothetical protein FLJ23188||	84561	NM_024628	NP_078904					
||BD1||BD-1||DEFB1||HBD-1||HBD1||beta defensin 1||DEFENSIN, BETA, 1||BETA-DEFENSIN 1 PRECURSOR||defensin, beta 1, preproprotein||	1672	NM_005218	NP_005209	Beta-defensin-1; has salt-dependent antimicrobial activity, may act in innate immunity	process|chemotaxis|E|GO:0006935|Proteome|10521347//biological process|immune response|E|GO:0006955|Proteome|10521347//biological process|antimicrobial humoral response|E|GO:0006960|Proteome|9038346//molecular function|antimicrobial response protein|E|GO:0003795|Proteome|9038346//biological process|G-protein linked receptor	organismal role|Pathogenic Invasion|E|Proteome|10521347//organismal role|Anti-pathogen response|NR|Proteome|9038346	has bactericidal activity (by similarity).	secreted.

H1||8-OXO-DGTPASE||EC 3.1.6.-||7,8-DIHYDRO-8-OXOGUANINE	TRIPHOSPHATASE||8-@OXO-7,8-DIHYDROGUANOSINE TRIPHOSPHATASE||NUDIX MOTIF 1||MutT HOMOLOG 1||NUCLEOSIDE DIPHOSPHATE-LINKED MOIETY X MOTIF, 1||mutT (E. coli) human homolog (8-oxo-7,8-dihydroguanosine triphosphatase)||nudix (nucleoside	4521	NM_002452	NP_002443	8-oxo-7,8-dihydroguanosine triphosphatase (8-oxo-dGTPase); may remove 8-oxoguanine nucleotides produced by oxidative damage; member of mutT family	molecular function|GTPase|E|GO:0003924|Proteome|7713500// biological process|DNA repair|NR|GO:0006281|Proteome|na//biological process|oxidative stress response|P|GO:0006979|Proteome|822 6881	cellular role|Cell stress|P|Prot eome|822688 1//cellular role|DNA repair|NR|Pro teome|77135 00//biochemical function|Hydr olase|E|Prote ome|7713500 .	antimutagenic. responsible for preventing misincorporation of 8-oxo-dgtp into dna thus preventing a:t to c:g transversions

biological process|cell adhesion|P|GO:0007155|Proteome|792	9347//molecular function|cell adhesion|P|GO:0005194|Proteome|792	9347//cellular component|plasma membrane|E|GO:0005886|Proteome|7929347//cellular component|membrane fraction|E|GO:0005624|Proteome|79293	9347//cellular component|tercellular junction|P|GO:0005911|Proteome|7929347	component of intercellular desmosome junctions. involved in the interaction of plaque proteins and intermediate filaments sin/agglutinin| mediating cell P|Proteome|7 cell adhesion. 929347//subc may ellular contribute to localization|C epidermal ell cell junction|NR|P positioning roteome|792 (stratification) 9347//molecu by mediating lar differential localization|In adhesiveness tegral between cells membrane|N that express R|Proteome|7 different isoforms.	‖CDHF3‖HT-CP‖DSC1‖DSC2‖DSC4‖DSC3‖DSC‖desmocollin 4‖DESMOCOLLIN 3 PRECURSOR‖desmocollin 3, isoform Dsc3b preproprotein ‖desmocollin 3, isoform Dsc3a preproprotein ‖	Desmocollin 3 (desmocollin 4); related to cadherin glycoproteins found in desmosomes	1825	NM_024423	NP_077741	type i membrane protein.

8||HBNF||NEGF1||PTN||HBGF8||HBNF-1||OSF-1||HB-GAM||HBNF1||PLEIOTROPHIN PRECURSOR||HEPARIN-BINDING GROWTH-ASSOCIATED MOLECULE||OSTEOBLAST SPECIFIC FACTOR 1||NEURITE OUTGROWTH-PROMOTING FACTOR, HEPARIN-BINDING||HEPARIN-BINDING GROWTH FACTOR 8||HEPARIN-BINDING NEURITE	5764	NM_002825	NP_002816	Pleiotrophin; heparin binding protein that induces mitogenic and neurite outgrowth activity	function|cytokine|NR|GO:0005125|Proteome|na//biological process|neurogenesis|E|GO:0007399|Proteome|2270483//molecular function|growth factor|NR|GO:0008083|Proteome|na//molecular function|heparin binding|NR|GO:0008201|Proteome|na//cellular component|extracellular space|E|GO:0005615|Proteome|10706604//molecular function|protein	molecular localization|Soluble|NR|Proteome|10706604//organismal role|Neuronal development|NR|Proteome|2270483//organismal role|Control of Cell Proliferation|E|Proteome|2270483//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|10706604	heparin binding mitogenic protein. has neurite extension activity.

one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	integral membrane protein.	||GJB6||EDH||NSRD1||HED||CX30||ED2||DFNA3||GAP JUNCTION BETA-6 PROTEIN||GAP JUNCTION PROTEIN, BETA-6||gap junction protein, beta 6 (connexin 30)|| ||KIAA0405||FLRT2||fibronectin leucine rich transmembrane protein 2||FIBRONECTIN-LIKE DOMAIN-CONTAINING LEUCINE-RICH TRANSMEMBRANE PROTEIN 2||	10804	NM_006783	NP_006774	Connexin 30; may have a role in intercellular transport and communication; member of a family of gap junction proteins	biological process|heart|GO:0007605|Proteome|10610709	molecular localization|Integral membrane|Proteome|10610709		
			23768	NM_013231	NP_037363				

Highly similar to rat growth and transformatio n-dependent protein	NP_055182	NM_014367	26355	molecular function|zinc binding|P|GO :0008270|Pro teome|96361 97//molecular function|carb onate dehydratase| E|GO:000408 9|Proteome|9 636197//cellu lar component|in tegral membrane protein|E|GO: 0016021|Prot eome|963619 7	Carbonic anhydrase XII (carbonate hydro-lyase); a zinc-containing enzyme that reversibly hydrates carbon dioxide; functions in cellular transport and metabolic processes	NP_001209	NM_001218	771	‖CA12‖CA-XII‖CA XIII‖carbonic dehydratase‖ EC 4.2.1.1‖TUM OR ANTIGEN HOM-RCC-3.1.3‖CARB ONATE DEHYDRAT ASE XIII‖carbonic anhydrase XII precursor‖	‖E2IG5‖hypo thetical protein, estradiol-induced‖

tumor suppressor. it blocks the growth, invasion, and metastatic									
	molecular function|serpin|NR|GO:0004868|Proteome|Family|NR|Protein	organismal role|Cellular process|cell motility|E|GO:0006928|Proteome|829096|molecular function|tumor suppressor|E|GO:0008181|Proteome|82290962	ility|NR|Protein|Inhibitor or repressor|E|Proteome|829096|molecular function|tumor suppressor|E|GO:0008181|Proteome|82290962	migration/motility|NR|Protein|Inhibitor or repressor|E|Proteome|829096|molecular function|tumor suppressor|E|GO:0008181|Proteome|82290962	properties of mammary tumors. as it does not undergo the s ai transition characteristic of active serpins, it exhibits no serine protease inhibitory activity.				
	Maspin; may be a serpin serine protease inhibitor, supresses tumor metastasis; member of the serpin family of serine protease inhibitors								
||PI5||SERPINB5||MASPIN||PRECURSOR||protease inhibitor 5 (maspin)||serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5||	5268	NM_002639	NP_002630						extracellular.

||D3S3194||BM28||cdc19||MCM2||KIAA0030||CCNL1||CDCL1||cyclin-like 1||NUCLEAR PROTEIN BM28||CELL DIVISION CYCLE-LIKE 1||DNA REPLICATION LICENSING FACTOR MCM2||minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin)||MINICHROMOSOME MAINTENANCE, S. CEREVISIAE, HOMOLOG OF, 2||	4171	NM_004526	NP_004517	Minichromosome maintenance protein; binds chromatin and regulates entry into S phase	component|nucleus|P|GO:0005634|Proteome|8175912//cellular component|chromatin|P|GO:0005717|Proteome|8798650//biological process|cell cycle|E|GO:0007049|Proteome|8175912//molecular function|DNA binding|P|GO:0003677|Proteome|8175912//biological process|DNA replication|E|GO:0006260|Proteome|8175912//molecular function|adenosinetriphosphatase|P|GO:0004002|Prot	cellular role|DNA synthesis|NR|Proteome|8798650//biochemical function|Hydrolase|P|Proteome|8175912//subcellular localization|Nuclear|P|Proteome|8175912//biochemical function|DNA-binding protein|P|Proteome|8175912//molecular localization|DNA-associated (direct or indirect)|P|Proteome|8175912	acts as a factor that allows the dna to undergo a single round of replication per cell cycle. required for the entry in s phase and for cell division.	nuclear (probable).

subcellular localization|Unspecified membrane|Proteome|10918388				
Protein with reduced expression in colorectal cancers	NP_057437	NM_016353	51201	||LOC51201||rec||
	NP_076404	NM_023915	53836	||GPR87||G protein-coupled receptor 87||

||GA17||dendritic cell protein||	10480	NM_006360	NP_006351									
||HSJ001348||cDNA for differentially expressed CO16 gene||	54742	BC001291		Has a region with low similarity to GML								
					6.4.1.3||PCCASE BETA SUBUNIT||pccBC COMPLEMENTATION GROUP||PROPIONYL-CoA CARBOXYLASE, BETA SUBUNIT||PROPANOYL-COA:CARBON DIOXIDE LIGASE BETA SUBUNIT||PROPIONYL-COA CARBOXYLASE BETA CHAIN, MITOCHONDRIAL PRECURSOR||propionyl Coenzyme A carboxylase, beta polypeptide||	5096	NM_000532	NP_000523	Propionyl Coenzyme A carboxylase (propanoyl-CoA:carbon-dioxide ligase (ADP-forming)) beta polypeptide; degrades branched-chain amino acids	cellular component|mitochondrion|P|GO:0005739|Proteome|8188292//biological process|fatty acid catabolism|NR|GO:0009062|Proteome|na//molecular function|propionyl-CoA carboxylase|P|GO:0004658|Proteome|8188292	biochemical function|Ligase|E|Proteome|8188292//cellular role|Amino-acid metabolism|NR|Proteome|3460076//subcellular localization|Mitochondrial|NR|Proteome|8188292	mitochondrial matrix.

||DCK||deoxycytidine kinase||EC 2.7.1.74||	1633	NM_000788	NP_000779	Deoxycytidine kinase; phosphorylates deoxyribonucleosides	molecular function|deoxycytidine kinase|E|GO:0004137|Proteome|1996353//biological process|pyrimidine nucleotide metabolism|E|GO:0006220|Proteome|1996353	biochemical function|Transferase|E|Proteome|1996353//biochemical function|Other kinase|E|Proteome|1996353	required for the phosphorylation of several deoxyribonucleosides and certain nucleoside analogs widely employed as antiviral and chemotherapeutic agents.	nuclear.
||DC42||hypothetical protein DC42||	81612	AK025746	NP_112183					

biological process|cell adhesion|P|GO:0007155|Proteome|9647 7647//cellular component|tight junction|P|GO:0005923|Proteome|9937 1503//cellular component|integral membrane protein|P|GO: 0016021|Proteome|99150 3//cellular component|integral plasma membrane protein|P|GO: 0005887|Proteome|964764 7	||SEMP1||CLAUDIN-1||CLDN1||CLD1||claudin 1||SENESCENCE-ASSOCIATED EPITHELIAL MEMBRANE PROTEIN 1||	9076	NM_021101	NP_066924	Claudin-1; protein with four transmembrane domains	subcellular localization|Cell|Proteome|9647 47647//subcellular localization|Basolateral|Proteome|96 47647	component of integral membrane protein.

||NOE1||AMY||pancortin 1||neuroblastoma protein||neuroblastoma (nerve tissue) protein||olfactomedin related ER localized protein||	10439	NM_014279	NP_478106	expressed in neuroblastoma cells	biological process|neurogenesis|P|GO:0007399|P|9501	organismal role|CNS-specific functions|E|P|roteome|9031|9501	seems to play an important role in regulating the production of neural crest cells by the neural tube (by similarity).	endoplasmic reticulum lumen (potential).		

||TOM20||MOM19||TOMM20-PENDING||KIAA0016||MAS20||MAS20P, S. CEREVISIAE, HOMOLOG OF||translocase of outer mitochondrial membrane 20 (yeast) homolog||	9804	NM_014765	NP_055580					
	5708	NM_002808	NP_002799	AP2||P97||S2||55.11 PROTEIN||TNFR-ASSOCIATED PROTEIN 2||PROTEASOME 26S, SUBUNIT 2||26S PROTEASOME SUBUNIT P97||26S PROTEASOME REGULATORY SUBUNIT S2||PROTEASOME 26S SUBUNIT, NON-ATPASE, 2||TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED PROTEIN 2||proteasome (prosome,	Non-ATPase subunit 2 of the 26S proteasome (prosome macropain); binds the type-1 tumor-necrosis-factor (TNF) receptor	cellular component|26S proteasome|E|GO:0005837|Proteome|8811196//cellular component|19S proteasome regulatory particle|P|GO:0005838|Proteome|8774743	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|8774743	binds to the intracellular domain of tumor necrosis factor type 1 receptor. the binding domain of trap1 and trap2 resides outside the death domain of tnfr1.

||TSA903||U MPK||UK||UR IDINE KINASE||uridine monophosphate kinase||	7371	NM_012474	NP_036606	component|membrane fraction|P|GO:0005624|Proteome|81247 22//biological process|mev alonate transport|P|GO:0015728|Proteome|142 9658//molecular function|mev alonate transporter|P|GO:0015130|Proteome|14 29658//cellular component|integral membrane Proton-monocarboxylate cotransporter; transports lactate and pyruvate; has a role in the Cori cycle	6566	NM_003051	NP_003042	proton-linked monocarboxylate transporter. catalyzes the rapid transport across the plasma membrane of many monocarboxylates such as lactate, pyruvate, branched-chain oxo acids derived from leucine, valine and isoleucine, and the ketone bodies acetoacetate, beta-hydroxybutyrate and acetate.
||SLC16A1||MCT||MCT1||MCT 1||MONOCARBOXYLATE TRANSPORTER 1||SOLUTE CARRIER FAMILY 16, MEMBER 1||solute carrier family 16 (monocarboxylic acid transporters), member 1||				molecular localization||integral membrane protein|P|GO:0016021|Proteome|81247 24722//biochemical function|Activity|8//biological process|monocarboxylic acid transport|E|GO:0015718|Proteome|81724				integral membrane protein. plasma membrane.

||TXN||TRX||SASP||thioredoxin||TRDX||ADF||ATL-DERIVED FACTOR||SURFACE ASSOCIATED SULPHYDRYL PROTEIN||	7295	NM_003329	NP_003320	Thioredoxin; has dithiol-disulfide oxidoreductase activity	function|thioredoxin|E|GO:0000008|Proteome|10947064//biological process|cell motility|E|GO:0006928|Proteome|10947064//biological process|cell proliferation|P|GO:0008283|Proteome|3170595//biological process|signal transduction|E|GO:0007165|Proteome|10947064//biological process|cell-cell signalling|E|GO:0007267|Proteome|10947064//biological process|anti	biochemical function|Oxidoreductase|NR|Proteome|3170595//organismal role|Anti-pathogen response|NR|Proteome|10947064//organismal role|Cell migration/motility|E|Proteome|10947064//organismal role|Cell-to-cell signalling|E|Proteome|10947064//organismal role|Control of Cell Proliferation|NR|Proteome|3170595	adf augments the expression of the interleukin-2 receptor tac (il2r/p55).	cytoplasmic.

||CBX1||MOD1||M31||HP1-BETA||HP1Hs-beta||CBX||MODIFIER 1 PROTEIN||CHROMOBOX PROTEIN HOMOLOG 1||heterochromatin protein p25 beta||HP1, DROSOPHILA, HOMOLOG OF, BETA||HETEROCHROMATIN PROTEIN 1 HOMOLOG BETA||chromobox homolog 1 (Drosophila HP1 beta)||	10951	NM_006807	NP_006798	Has chromodomain and heterochromatin binding domains	cellular component|nucleoplasm|E|GO:0005654|Proteome|9169582//cellular component|heterochromatin|E|GO:0005720|Proteome|9169582//molecular function|chromatin binding|E|GO:0003682|Proteome|9169582	subcellular localization|Nuclear|E|Proteome|9169582//biochemical function|DNA-binding protein|P|Proteome|9169582//cellular role|Chromatin/chromosome structure|P|Proteome|9169582//molecular localization|DNA-associated (direct or indirect)|E|Proteome|9169582	component of heterochromatin. may interact with lamin b receptor (lbr). this interaction can contribute to the association of the heterochromatin with the inner nuclear membrane.	nuclear (potential).

||KIAA0024||PSSA||PTDSS1||EC 2.7.8.-||phosphatidylserine synthase 1||PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-)||	9791	NM_014754	NP_055569	base-exchange reaction between free l-serine and the polar head groups of pre-existing phospholipids. it can utilize phosphatidylcholine as a phosphatidyl donor. it can also catalyzes the choline and ethanolamine base-exchange reactions.	integral membrane protein.

					component|endosome|EIGO:0005768|Proteome|839 4993//biological process|iron transport|NR|GO:0006826|Proteome|na//biological process|iron homeostasis|PIGO:0006879|Proteome|10192390//molecular function|transferrin receptor|PIGO:0004998|Proteome|10192390//cellular component|tegral plasma membrane protein|PIGO: 0005887|Proteome|6096955	uptake of iron occurs via receptor-mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. endosomal acidification leads to iron release. the apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral ph and the concomitant loss of affinity
||P90||TR||TFRC||TFR||CD71||T9||TRFR||ANTIGEN CD71||TRANSFERRIN RECEPTOR PROTEIN||transferrin receptor (p90, CD71)||	7037	NM_003234	NP_003225	Transferrin receptor; binds and internalizes the iron carrier transferrin; highly similar over the N-terminal region to murine Trfr	ptor (protein translocation) |Proteome|6273413	type ii membrane protein. the stfr isoform is secreted.

||A4||PLP2||A4-LSB||A4 differentiation-dependent protein||DIFFERENTIATION-DEPENDENT PROTEIN A4||INTESTINAL MEMBRANE A4 PROTEIN||proteolipid protein 2 (colonic epithelium-enriched)||	5355	NM_002668	NP_002659	Proteolipid 2; may multimerize to form an ion channel	process|ion transport|P|GO:0006811|Proteome|9124532//molecular function|ion transporter|P|GO:0015075|Proteome|9124532//cellular component|membrane fraction|P|GO:0005624|Proteome|9124532//cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|9124532//cellular component|endoplasmic reticulum membrane|E|GO:0005789|Proteome|9124532	molecular localization|Integral membrane|E|Proteome|9124532//subcellular localization|Unspecified membrane|P|Proteome|9124532//biochemical function|Channel [passive transporter]|P|Proteome|9124532	may play a role in cell differentiation in the intestinal epithelium.	integral membrane protein.

implicated in the hormonal control of several regulatory proteins including glycogen synthase, myb, and the transcription factor c-jun. it phosphorylates c-jun at proximal to its dna-binding domain; reducing dna-binding affinity.	||GSK3B||GSK-3 BETA||EC 2.7.1.37||GLYCOGEN SYNTHASE KINASE-3 BETA||GLYCOGEN SYNTHASE KINASE 3-BETA||glycogen synthase kinase 3 beta||	2932	NM_002093	NP_002084	Glycogen synthase kinase 3b; protein-serine kinase that phosphorylates regulatory proteins	biological process|glycogen metabolism|EC|GO:0005977 |Proteome|798 0435//molecular function|glycogen synthase kinase 3|E|GO:0004696|Proteome|7980435	biochemical function|Transferase|NR|Proteome|798 0435//organismal role|Cell fate specification| NR|Proteome|7980435

RZ1||RPTPB||HPTP-ZETA||PTP18||RPTP-BETA||PTPRZ||R-PTP-ZETA||EC 3.1.3.48||PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR||Protein-tyrosine phosphatase, receptor-type, zeta-1, polypeptide||protein tyrosine phosphatase, receptor-type, Z polypeptide 1||protein tyrosine phosphatase, receptor-type, zeta	process|protein dephosphorylation|GO:0006470|Protein|1323835|cellular component|integral plasma membrane protein|P|GO:0005887|Protein|838752|biological process|central nervous system development|GO:0007417|Proteome|8387522|molecular function|transmembrane receptor protein phosphatase Z1; similar to carbonic anhydrases in the extracellular domain	5803	NM_002851	NP_002842	Receptor-type protein tyrosine phosphatase receptor type Z1; similar to carbonic anhydrases in the extracellular domain	cular membrane receptor protein tyrosine phosphatase| 1|Proteome|1323835	tegral membrane|P|Proteome|87522//biochemical function|Receptor|GO:000500 1|Proteome|1323835	biochemical function|Hydrolase|E|Proteome|87522//biochemical function|Receptor|GO:000500 (signalling)|P|Proteome|87522	may be involved in the regulation of specific development al processes in the cns.	type i membrane protein.

||KIAA0343||NRCAM||Bravo||neuronal cell adhesion molecule||	4897	NM_005010	NP_005001	Neuronal cell adhesion molecule (Bravo); functions as a cell surface protein; member of the immunoglobulin superfamily	biological process|cell adhesion|P|GO:0007155|Proteome|8812479//molecular function|cell adhesion|NR|GO:0005194|Proteome|na//molecular function|tumor suppressor|P|GO:0008181|Proteome|8812479//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|8812479	organismal role|Neuronal development|P|Proteome|8812479//biochemical function|Adhesin/agglutinin|P|Proteome|8812479//molecular localization|Integral membrane|P|Proteome|8812479	
||TYMK||TMPK||DTYMK||CDC8||EC 2.7.4.9||DTMP KINASE||deoxythymidylate kinase (thymidylate kinase)||	1841	NM_012145	NP_036277	Deoxythymidylate kinase (dTMP kinase); phosphorylates dTMP to form dTDP	biological process|cell cycle|E|GO:0007049|Proteome|8024690//biological process|DNA metabolism|NR|GO:0006259|Proteome|na//biological process|cell proliferation|P|GO:0008283|Proteome|8024690//molecular function|thymidylate kinase|E|GO:0004798|Proteome|8024690	biochemical function|Transferase|E|Proteome|8024690//biochemical function|Other kinase|E|Proteome|8024690	catalyzes the conversion of dtmp to dtdp.

||CCA||FBN2|| FIBRILLIN 2 PRECURSOR||CONTRACTURAL ARACHNODACTYLY, CONGENITAL||BEALS SYNDROME FIBRILLIN 2||congenital contractural arachnodactyly (Marfanoid-like)||fibrillin 2 (congenital contractural arachnodactyly)||	2201	NM_001999	NP_001990	Fibrillin 2; ECM protein, regulates formation and maintenance of microfibrils	cellular component|extracellular matrix|E|GO:0005578|Proteome|8120105//biological process|histogenesis and organogenesis|P|GO:0007397|Proteome|8120105//biological process|embryogenesis and morphogenesis|P|GO:0007345|Proteome|7493032//molecular function|extracellular matrix structural protein|E|GO:0005201|Proteome|8120105	organismal role|Extracellular matrix component|NR|Proteome|8120105//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|8120105//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|8120105//subcellular localization|Extracellular matrix (cuticle and basement membrane)|NR|Proteome|8120105	structural component of connective tissue microfibrils that binds calcium. fibrillin-2-containing microfibrils regulate the early process of elastic fiber assembly.

||hypothetical protein MGC12966||	84792	NM_032706	NP_116095	3A2||4T2HC|| CD98||4F2H C||4F2||NAC AE||CD98 ANTIGEN||C D98 HEAVY CHAIN||CD9 8 MONOCLON AL ANTIBODY 44D7||4F2 HEAVY CHAIN ANTIGEN||4F 2 CELL- SURFACE ANTIGEN HEAVY CHAIN||SOL UTE CARRIER FAMILY 3, MEMBER 2||LYMPHOC YTE ACTIVATION ANTIGEN 4F2 LARGE SUBUNIT||A NTIGEN	6520	NM_002394	NP_002385	involved in normal and neoplastic cell growth.	type ii membrane protein.

P5G||ATP5G1||EC 3.6.3.14||ATPASE PROTEIN 9||ATPASE SUBUNIT C||ATP SYNTHASE PROTEOLIPID P1||ATP SYNTHASE LIPID-BINDING PROTEIN, MITOCHONDRIAL PRECURSOR||MITOCHONDRIAL ATP SYNTHASE, SUBUNIT C, ISOFORM 1||MITOCHONDRIAL ATP SYNTHASE, SUBUNIT 9, ISOFORM 1||ATP SYNTHASE, H+					function|transporter|NR|GO:0005215|Proteome|na//cellular component|membrane fraction|NR|GO:0005624|Proteome|na//cellular component|mitochondrial inner membrane|NR|GO:0005743|Proteome|na//cellular component|hydrogen-transporting ATP synthase|P|GO:0005753|Proteome|8328972//molecular function|hydrogen-transporting two-sector	biochemical function|Hydrolase|NR|Proteome|8328972//subcellular localization|Mitochondrial|NR|Proteome|8328972//molecular localization|Integral membrane|NR|Proteome|8328972//subcellular localization|Unspecified membrane|NR|Proteome|8328972//biochemical function|Active transporter, primary|NR|Proteome|8328972		
516	NM_005175	NP_005166	Isoform 1 (P1) of subunit c, H+-translocating subunit of F0 ATP synthase; catalyzes the synthesis of ATP during oxidative phosphorylation				this protein is one of the chains of the nonenzymatic membrane component (f0) of mitochondrial atpase.	mitochondrial membrane.

||IL1RN||IRAP||ICIL-1RA||IL-1RN||IL1RA||interleukin 1 receptor antagonist||INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR||	3557	NM_000577	NP_000568	interleukin 1 receptor antagonist; binds to and inhibits the IL-1 receptor; member of the interleukin-1 (IL-1) family	cellular component|intracellular|NR|GO:0005622|Proteome|na//cellular component|extracellular space|P|GO:0005615|Proteome|1385987//biological process|inflammatory response|NR|GO:0006954|Proteome|na//molecular function|interleukin-1 receptor antagonist|E|GO:0005152|Proteome|2139180	organismal role|Anti-pathogen response|NR|Proteome|1386337//biochemical function|Inhibitor or repressor|E|Proteome|10786823//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|1385987	il-1ra inhibits the activity of il-1 by binding to its receptor. il-1ra has no il-1 like activity.	secreted (isoform 1) or intracellular (isoforms 2, 3 and 4).

molecular function|syndecan|P|GO:0015023|Proteome|2324102	//cellular component|integral plasma membrane|proteoglycan|P|GO:0005887|Proteome|2324102	molecular localization|integral membrane|N|Proteome|2324102	cell surface proteoglycan that bears both heparan sulfate and chondroitin sulfate and	||SDC1||CD138||SYND1||SDC||syndecan 1||CD138 ANTIGEN||SYNDECAN-1 PRECURSOR||	Syndecan; mediates cell behaviors like cell adhesion, action of growth factors	6382	NM_002997	NP_002988	that links the cytoskeleton to the interstitial matrix.	type i membrane protein.

||PLD1||HPLD1||PLD1||EC 3.1.4.4||phospholipase D1, phophatidylcholine-specific||phospholipase D1, phosphatidylcholine-specific||CHOLINE PHOSPHATASE 1||PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D1||	5337	NM_002662	NP_002653	ADP ribosylation factor-activated phosphatidylcholine-specific phospholipase D1; stimulated by phosphatidylinositol 4,5-bisphosphate and inhibited by oleate	component|membrane|E|GO:0016020|Proteome|8530346//biological process|chemotaxis|P|GO:0006935|Proteome|10848592//molecular function|phospholipase D|E|GO:0004630|Proteome|8530346//biological process|phospholipid metabolism|NR|GO:0006644|Proteome|na//biological process|RAS protein signal transduction|P|GO:0007265|Proteome|10848592//biological	biochemical function|Hydrolase|E|Proteome|10747870//organismal role|Cell migration/motility|P|Proteome|10848592//subcellular localization|Unspecified membrane|E|Proteome|8530346	implicated as a critical step in numerous cellular pathways, including signal transduction, membrane trafficking, and the regulation of mitosis. may be involved in the regulation of perinuclear intravesicular membrane traffic (by similarity).	perinuclear regions: endoplasmic reticulum, golgi apparatus and late endosomes (by similarity).

2||LAMPB||LAMP2||CD107B	3920	NM_013995	NP_054701	Lysosomal membrane glycoprotein 2	cellular component|lysosomal membrane|GO:0005887|Proteome|319860|5	molecular localization|integral membrane protein|PGO:0016021|Proteome|203272|4	lysosome, adhesion when expressed on the cell surface (plasma membrane), and intracellular signal transduction.	type i membrane protein. lysosomal. this protein shuttles between lysosomes, endosomes, and the plasma membrane.	implicated in tumor cell metastasis. may function in protection of the lysosomal membrane from autodigestion, maintenance of the acidic environment of the	ANTIGEN||Lysosome-associated membrane protein-2||LYSOSOME-ASSOCIATED MEMBRANE PROTEIN 2||LYSOSOME-ASSOCIATED MEMBRANE PROTEIN B||lysosomal-associated membrane protein 2 precursor||LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2

||CLECSF2|| HP10085||ACL||ACTIVATION-INDUCED C-TYPE LECTIN||LECTIN, C-TYPE, ACTIVATION-INDUCED||LECTIN, C-TYPE, SUPERFAMILY MEMBER 2||C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)||	9976	NM_005127	NP_005118	Activation-induced C-type lectin 2	molecular function|lectin|P|GO:0005530|Proteome|9038101//molecular function|lymphocyte antigen|P|GO:0005557|Proteome|90381 01//biological process|antimicrobial humoral response|P|GO:0006960|Proteome|903 8101//cellular component|in tegral plasma membrane protein|P|GO: 0005887|Proteome|903810 1	organismal role|Anti-pathogen response|P|P roteome|903 8101//molecular|in localization|integral membrane|P| Proteome|90 38101	type ii membrane protein (probable).

ALPHA||PI3K ||PIK3CA||EC 2.7.1.137||PT DINS-3- KINASE P110||phosph oinositide-3- kinase, catalytic, alpha polypeptide|| PI3-KINASE P110 SUBUNIT ALPHA||phos phatidylinosit ol 3-kinase, catalytic, alpha polypeptide|| PHOSPHATI DYLINOSITO L 3-KINASE, CATALYTIC, 110-KD, ALPHA||PHO SPHATIDYLI NOSITOL 3- KINASE CATALYTIC SUBUNIT,	5290	NM_006218	NP_006209	Catalytic subunit of phosphatidyli nositol 3- kinase	biological process|onco genesis|PIG O:0007048|P roteome|991 6799	phosphorylat es ptdins, ptdins4p and ptdins(4,5)p2 with a preference for ptdins(4,5)p2.

||CTSL2||CTSV||CTSU||CATL2||CATHEPSIN U||CATHEPSIN V||EC 3.4.22.43||CATHEPSIN L2 PRECURSOR||	1515	NM_001333	NP_001324	Cathepsin L2 (cathepsin V); cysteine (thiol) protease	molecular function|cathepsin L|P|GO:0004217|Proteome|9563472//molecular function|cysteine-type peptidase|E|GO:0008234|Proteome|9563472	biochemical function|Hydrolase|E|Proteome|9563472//biochemical function|Protease (other than proteasomal)|E|Proteome|9563472	is a cysteine protease. may have an important role in corneal physiology.	lysosomal (potential).

||hypothetical protein FLJ20105||	54821	AK056494	NP_060139	May mediate protein-protein interactions; contains a TPR (tetratricopeptide repeat) domain		
||CHST2||N-ACETYLGLUCOSAMINE-6-O-SULFOTRANSFERASE||C6ST||GlcNAc-6-O-SULFOTRANSFERASE||CARBOHYDRATE SULFOTRANSFERASE 2||carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2||carbohydrate (chondroitin 6/keratan) sulfotransferase 2||	9435	AB021124	NP_004258	N-acetylglucosamine-6-O-sulfotransferase; may play a role in cell-surface antigen and carbohydrate structure production	molecular function|sulfotransferase|E|GO:0008146|Proteome|9722682//biological process|inflammatory response|P|GO:0006954|Proteome|10049591//biological process|developmental processes|P|GO:0007275|Proteome|9722682	biochemical function|Transferase|E|Proteome|9722682

||GS-X||ABC29||ABCC1||ABCC||multidrug resistance protein||multiple drug resistance-associated protein||MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1||multiple drug resistance protein 1||ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 1||ATP-binding cassette, sub-family C (CFTR/MRP), member 1||ATP-	4363	NM_004996	NP_063957	Multiple drug resistance protein; ABC (ATP-binding cassette) transporter	function|ATP binding|P|GO:0005524|Proteome|1360704//molecular function|transporter|P|GO:0005215|Proteome|1360704//biological process|drug resistance|P|GO:0009315|Proteome|1360704//cellular component|membrane fraction|P|GO:0005624|Proteome|1360704//biological process|small molecule transport|P|GO:0006832|Proteome|1360704//cellular component|integral plasma membrane	biochemical function|Hydrolase|P|Proteome|1360704//molecular localization|Integral membrane|P|Proteome|1360704//biochemical function|ATP-binding cassette|NR|Proteome|1360704//subcellular localization|Unspecified membrane|P|Proteome|1360704//biochemical function|Active transporter, primary|P|Proteome|1360704	may participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly.	integral membrane protein.

||HHM||PTHRP[107-139]||PTH-RP||OSTEOSTATIN||PTHLH||PTHRP||PTH-RELATED PROTEIN||parathyroid hormone-like hormone||PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR||PTHR, FORMERLY HUMORAL HYPERCALCEMIA OF MALIGNANCY||	5744	NM_002820	NP_002811	Precursor of parathyroid hormone-related hormone; regulates epidermal development; strongly similar to murine Pthlh	process|pregnancy|P|GO:0007565|Proteome|10828849//cellular component|cytoplasm|E|GO:0005737|Proteome|10803599//biological process|excretion|NR|GO:0007588|Proteome|na//cellular component|nucleolus|NR|GO:0005730|Proteome|na//biological process|oncogenesis|NR|GO:0007048|Proteome|na//molecular function|peptide hormone|P|GO:0005180|Proteome|270	localization|Soluble|E|Proteome|8641188//subcellular localization|Nuclear|NR|Proteome|10803599//subcellular localization|Cytoplasmic|E|Proteome|10803599//organismal role|Cell-to-cell signalling|E|Proteome|2549037//subcellular localization|Nuclear nucleolus|E|Proteome|10947864//organismal role|Control of Cell Proliferation|E|Proteome|10773581//org	osteostatin is a potent inhibitor of osteoclastic bone resorption.	secreted.

||UBE2C||ubiquitin-conjugating enzyme E2C||UBIQUITIN-CONJUGATING ENZYME UBCH10||ubiquitin carrier protein E2-C||	11065	NM_007019	NP_008950	Subunit of a complex with ubiquitin ligase activity; complex that exhibits cyclin-selective ubiquitin ligase activity	process|protein modification|E|GO:0006464|Proteome|9122200//biological process|degradation of cyclin|E|GO:0008054|Proteome|9122200//molecular function|ubiquitin--protein ligase|P|GO:0004842|Proteome|9122200//biological process|positive control of cell proliferation|E|GO:0008284|Proteome|9122200//biological process|ubiquitin-dependent protein	biochemical function|Ligase|E|Proteome|9122200//cellular role|Protein degradation|E|Proteome|9122200//organismal role|Control of Cell Proliferation|E|Proteome|9122200//biochemical function|Protein conjugation factor|E|Proteome|9122200	catalyzes the covalent attachment of ubiquitin to other proteins. required for the destruction of mitotic cyclins.
||S9||p44.5||PSMD11||PROTEASE 26S, SUBUNIT 9||PROTEASOME 26S SUBUNIT, NON-ATPase, 11||proteasome (prosome, macropain) 26S subunit, non-ATPase, 11||	5717	NM_002815	NP_002806	Non-ATPase subunit of the 26S proteasome (prosome macropain)	cellular component|26S proteasome|E|GO:0005837|Proteome|9119060	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|9119060	
||AWS||JAGL1||HJ1||JAG1||AGS||AHD||jagged1 (Alagille syndrome)||jagged 1 precursor||jagged 1 (Alagille syndrome)||	182	NM_000214	NP_000205				

‖RIT‖RIBB‖ROC1‖Ric (Drosophila)-like, expressed in many tissues‖	6016	NM_006912	NP_008843	Member of the ras subfamily of GTP binding proteins; binds calmodulin; lacks a C-terminal prenylation site	molecular function|GTP binding|E|GO:0005525|Proteome|8824319//cellular component|plasma membrane|E|GO:0005886|Proteome|8824319//molecular function|calmodulin binding|E|GO:0005516|Proteome|8918462//biological process|signal transduction|P|GO:0007165|Proteome|8918462	biochemical function|Hydrolase|P|Proteome|8918462//biochemical function|GTP-binding protein/GTPase|P|Proteome|8918462//biochemical function|Small molecule-binding protein|E|Proteome|8918462	
‖PSK-J3‖CMM3‖CDK4‖MGC14458‖EC 2.7.1.-‖cyclin-dependent kinase 4‖melanoma cutaneous malignant, 3‖CELL DIVISION PROTEIN KINASE 4‖CELL DIVISION KINASE 4 MELANOMA, CUTANEOUS MALIGNANT, 3‖	1019	NM_000075	NP_443710	Cyclin-dependent protein kinase 4; required for cell cycle progression, phosphorylates pRb and inactivates its repressor function	process|oncogenesis|E|GO:0007048|Proteome|7652577//biological process|cell cycle control|E|GO:0000074|Proteome|7652577//biological process|cell proliferation|E|GO:0008283|Proteome|10499802//biological process|mitotic G1/S transition|E|GO:0000082|Proteome|10499802//molecular function|cyclin-dependent protein kinase|E|GO:0004693|Proteome|104998	biochemical function|Transferase|E|Proteome|10748174	probably involved in the control of the cell cycle.

||TOPK||spermatogenesis-related protein kinase||PDZ-binding kinase; T-cell originated protein kinase||	55872	NM_018492	NP_060962					
||FS||FST||ACTIVIN-BINDING PROTEIN||FOLLISTATIN PRECURSOR||follistatin isoform FST317 precursor||follistatin isoform FST344 precursor||	10468	NM_006350	NP_037541	Follistatin; inhibits the release of follicle-stimulating hormone (FSH)	biological process|developmental processes|P|GO:0007275|Proteome|9828086	organismal role|Reproduction|NR|Proteome|3380788//biochemical function|Inhibitor or repressor|NR|Proteome|3380788	binds directly to activin and functions as an activin antagonist. specific inhibitor of the biosynthesis and secretion of pituitary follicle stimulating hormone (fsh).	secreted.

cellular component|cytoplasm|NR|GO:0005737|Proteome|na//molecular function|thymidine kinase|P|GO:0004797|Proteome|333550 3//biological process|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|P|GO:0006139|Proteome|3355 03	||TK1||Thymidine kinase-1||EC 2.7.1.21||THYMIDINE KINASE, CYTOSOLIC||THYMIDINE KINASE, SOLUBLE||thymidine kinase 1, soluble||	7083	NM_003258	NP_003249	Thymidine kinase, cytosolic form; generates thymidylate for DNA synthesis				subcellular localization|Cytoplasmic|NR|Proteome|335503	cytoplasmic.

||MPR-S15||DC37||RPMS15||MRPS15||FLJ11564||mitochondrial ribosomal protein S15||28S ribosomal protein S15, mitochondrial||	64960	NM_031280	NP_112570					
F3||LTB4H||CYP4F3||CYPIVF3||EC 1.14.13.30||cytochrome P450-LTB-omega||leukotriene-B4 20-monooxygenase||LTB4 OMEGA-HYDROXYLASE||LEUKOTRIENE-B4 OMEGA-HYDROXYLASE||CYTOCHROME P450 4F3||LEUKOTRIENE B4 OMEGA-HYDROXYLASE||leukotriene B4 omega hydroxylase (cytochrome P450, subfamily IVF)||cytochr	4051	NM_000896	NP_000887	Polymorphonuclear leukocyte leukotriene B4 omega-hydroxylase; converts leukotriene B4 into the less active 20-hydroxy-leukotriene B4	molecular function|monooxygenase|E|GO:0004497|Proteome|8486631//biological process|leukotriene metabolism|P|GO:0006691|Proteome|8486631	biochemical function|Oxidoreductase|NR|Proteome|8486631//organismal role|Anti-pathogen response|NR|Proteome|8486631	cytochromes p450 are a group of heme-thiolate monooxygenases. this enzyme requires molecular oxygen and nadph for the omega-hydroxylation of ltb4. it is inhibited by carbon monoxide (co).	membrane-bound. endoplasmic reticulum.

||UHRF1||FLJ21925||Np95||transcription factor ICBP90||ubiquitin-like, containing PHD and RING finger domains, 1||	29128	NM_013282	NP_037414	DNA-binding protein; may regulate expression of topoisomerase 2 alpha	biological process|cell proliferation|P|GO:0008283|Proteome|10646863//molecular function|transcription factor|P|GO:0003700|Proteome|1868030//molecular function|RNA polymerase II transcription factor|E|GO:0003702|Proteome|10646863//biological process|transcription regulation from Pol II promoter|E|GO:0006357|Proteome|10646863	cellular role|Pol II transcription|P|Proteome|10646863//biochemical function|DNA-binding protein|E|Proteome|10646863//organismal role|Control of Cell Proliferation|P|Proteome|1868030//molecular localization|DNA-associated (direct or indirect)|E|Proteome|10646863

||HSPC163 protein||	29097	NM_014184	NP_054903					
||SPUF||secreted protein of unknown function||	29937	NM_013349	NP_037481	Low similarity to a region of PMBP, which is a putative steroid membrane receptor				
||RASL2-8||LPS||RAN||ARA24||TC4||RAN GTPASE||ras-related nuclear protein||ANDROGEN RECEPTOR-ASSOCIATED PROTEIN 24||GTP-BINDING NUCLEAR PROTEIN RAN||RAN, member RAS oncogene family||RAN, member RAS oncogene family||	5901	NM_006325	NP_006316	Member of the ras family of GTP binding proteins; couples DNA synthesis completion to mitosis; induces spindle formation; involved in nuclear transport of RNA and proteins; interacts with polyglutamate repeats of the androgen receptor	process|mitosis|P|GO:0007067|Proteome|8421051//cellular component|nucleus|NR|GO:0005634|Proteome|na//cellular component|chromatin|P|GO:0005717|Proteome|10408446//cellular component|nuclear pore|NR|GO:0005643|Proteome|na//biological process|DNA metabolism|P|GO:0006259|Proteome|8421051//biological process|cell cycle control|NR|G	role|DNA synthesis|P|Proteome|8421051//biochemical function|Hydrolase|NR|Proteome|10408446//subcellular localization|Nuclear|NR|Proteome|10400640//cellular role|Nuclear-cytoplasmic transport|P|Proteome|7603572//biochemical function|GTP-binding protein/GTPase|NR|Proteome|10408446//molecular localization|DNA-associated (direct or indirect)|NR|	enhances ar-mediated transactivation. transactivation decreases as the poly-gln length within ar increases.	nuclear; becomes dispersed throughout the cytoplasm during mitosis.

||HSI||ARL1||ALDRLn||HIS||ARL-1||AKR1B10||AKR1B11||AKR1B12||HSI REDUCTASE||aldose reductase-like 1||HUMAN SMALL INTESTINE REDUCTASE||aldo-keto reductase family 1, member B11 (aldose reductase-like)||aldo-keto reductase family 1, member B10 (aldose reductase)||	57016	NM_020299	NP_064695	Aldo-keto reductase 1B10 (aldose reductase-like, human small intestine reductase); reduces aliphatic and aromatic aldehydes and, less so, hexoses; may detoxify reactive digested aldehydes, and may act in steroid metabolism	process|digestion|P|GO:0007586|Proteome|9565553//biological process|steroid metabolism|P|GO:0008202|Proteome|9565553//molecular function|aldehyde reductase|E|GO:0004032|Proteome|9565553//biological process|aldehyde metabolism|E|GO:0006081|Proteome|9565553//molecular function|aldo-keto reductase|P|GO:0004033|Proteome|9765553	biochemical function|Oxidoreductase|E|Proteome|9565553	
||ON||SPARC||SPARC PRECURSOR||BASEMENT MEMBRANE PROTEIN BM-40||Osteonectin (secreted protein, acidic, cysteine-rich)||secreted protein, acidic, cysteine-rich (osteonectin)||SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE||	6678	NM_003118	NP_003109	Osteonectin; binds collagen and hydroxyapatite	biological process|ossification|P|GO:0001503|Proteome|7034958//molecular function|calcium binding|E|GO:0005509|Proteome|7034958//molecular function|collagen binding|E|GO:0005518|Proteome|7034958//cellular component|extracellular matrix|E|GO:0005578|Proteome|7034958	organismal role|Bone Development and Maintenance|P|Proteome|7034958//biochemical function|Small molecule-binding protein|E|Proteome|7034958//subcellular localization|Extracellular matrix (cuticle and basement membrane)|E|Proteome|7034958	regulate cell growth through interactions with the extracellular matrix and cytokines. binds calcium and copper, several types of collagen, albumin, thrombospondin, pdgf and cell membranes. there are two calcium binding sites; a acidic domain that binds 5 to 8 ca++ with a low affinity and a ef-hand loop that binds a ca++ ion with a high affinity.

DPKA||NM23||NM23-H1||NME1||NDK A||EC 2.7.4.6||NUCLEOSIDE DIPHOSPHATE KINASE-A||NDP KINASE A||METASTASIS INHIBITION FACTOR NM23||NUCLEOSIDE DIPHOSPHATE KINASE A||non-metastatic cells 1 protein||TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN||NONMETASTATIC PROTEIN	4830	NM_000269	NP_000260	Transcription factor and nucleoside diphosphate kinase; has a role in the transcriptional regulation of c-myc expression	biochemical function|Transferase|E|Proteome|83927 52//biochemical function|Other kinase|E|Proteome|839275 2//cellular role|Pol II transcription|E|Proteome|8392752//biochemical function|Inhibitor or repressor|NR|Proteome|8392752	major role in the synthesis of nucleoside triphosphates other than atp.	nuclear and cytoplasmic.

AK055356	||LOC51651|| CGI-147 protein||	51651	AK057033	NP_057161	||SCD||DELTA(9)-DESATURASE||ACYL-COA DESATURASE||EC 1.14.99.5||stearoyl-CoA desaturase (delta-9-desaturase)|| FATTY ACID DESATURASE||	6319	NM_005063	NP_005054	Stearoyl-coenzyme A desaturase; functions in the synthesis of unsaturated fatty acids	molecular function|stearoyl-CoA 9-desaturase|P|GO:0004768|Proteome|10229681	biochemical function|Oxidoreductase|N|Proteome|7909540	terminal component of the liver microsomal stearyl-coa desaturase system, that utilizes o(2) and electrons from reduced cytochrome b(5) to catalyze the insertion of a double bond into a spectrum of fatty acyl-coa substrates among which palmitoyl-coa and stearoyl-coa.	integral membrane protein. endoplasmic reticulum (probable).

HUMNDME|| NADP-ME||pyruvic-malic carboxylase|| EC 1.1.1.40||Malic enzyme, cytoplasmic|| NADP-dependent malic enzyme||MALIC ENZYME, SOLUBLE||malic enzyme 1, soluble||MALATE DEHYDROGENASE, NADP(+)-DEPENDENT, SOLUBLE||cytosolic malic enzyme 1||MALIC ENZYME, NADP(+)-DEPENDEN	4199	NM_002395	NP_002386	Cytosolic NADP(+)-dependent malic enzyme; catalyzes the oxidative decarboxylation of malate to form pyruvate	component|cytosol|NR|GO:0005829|Proteome|na//biological process|malate metabolism|NR|GO:0006108|Proteome|na//molecular function|electron transporter|EC GO:0005489|Proteome|76 22060//biological process|carbohydrate metabolism|NR|GO:0005975|Proteome|na//biological process|tricarboxylic acid cycle|NR|GO:0006099|Proteome|na//molecular function|malate	biochemical function|Oxidoreductase|Proteome|76 22060//subcellular localization|Cytoplasmic|NR|Proteome|8187880	cytoplasmic.

9||CLG4B||G ELB||MMP9|| GELATINAS E, 92-KD||macroph age gelatinase||E C	4318	NM_004994	NP_004985	Type IV collagenase (gelatinase B); matrix metalloprotea se that digests type IV and type V collagen	molecular function|colla genase|E|GO :0008133|Pro teome|25518 98//molecular function|zinc binding|P|GO :0008270|Pro teome|25518 98//cellular component|e xtracellular space|E|GO: 0005615|Prot eome|25189 8//biological process|prote olysis and peptidolysis|E |GO:0006508 |Proteome|25 51898	biochemical function|Hydr olase|E|Prote ome|2551898 //cellular role|Protein degradation| E|Proteome|2 551898//orga nismal role|Extracell ular matrix maintenance| NR|Proteome |2551898//bio chemical function|Prot ease (other than proteasomal)| E|Proteome|2 551898//subc ellular localization|E xtracellular (excluding cell wall)|NR|Prot eome|25189 8	could play a role in bone osteoclastic resorption.

||P105MCM|| MCM6||Mis5|| DNA REPLICATION LICENSING FACTOR MCM6||MINI CHROMOSOME MAINTENANCE, S. POMBE, HOMOLOG OF, 6||minichromosome maintenance deficient (mis5, S. pombe) 6||	4175	NM_005915	NP_005906	may be involved in the control of a single round of dna replication during s phase. binds to chromatin during g1 and detach from it during s phase as if it licenses the chromatin to replicate.	nuclear (by similarity).

||LIG||HIP-2||HIP2||ubiquitin-protein ligase||EC 6.3.2.19||UBIQUITIN-CONJUGATING ENZYME E2-25K||HUNTINGTIN-INTERACTING PROTEIN 2||ubiquitin carrier protein||huntingtin interacting protein 2||ubiquitin-conjugating enzyme E2-25 KDA||	3093	NM_005339	NP_005330	Ubiquitin-conjugating enzyme	function|ubiquitin--protein ligase|P|GO:0004842|Proteome|8702625//molecular function|ubiquitin conjugating enzyme|P|GO:0004840|Proteome|8702625//biological process|ubiquitin-dependent protein degradation|P|GO:0006511|Proteome|8702625//biological process|small ubiquitin-related protein 1 conjugation|E|GO:0006485|Proteome|8702625	biochemical function|Ligase|E|Proteome|8702625//cellular role|Protein degradation|P|Proteome|8702625//organismal role|CNS-specific functions|P|Proteome|8702625//biochemical function|Protein conjugation factor|E|Proteome|8702625	catalyzes the covalent attachment of ubiquitin to other proteins. mediates the selective degradation of short-lived and abnormal proteins. ubiquitinates huntingtin.	cytoplasmic.

993	NM_001789	NP_001780	Protein tyrosine and threonine phosphatase (PTPase); acts as a protein tyrosine and threonine phosphatase (PTPase); mediates cell cycle progression by activating mitotic CDKs	biological process|cell cycle control|P|GO: 0000074|Prot eome|183697 8//biological process|regul ation of CDK activity|P|GO: 0000079|Prot eome|766763 6	organismal role|Control of Cell Proliferation| NR|Proteome |7667636	‖protein-tyrosine-phosphatase|EC 3.1.3.48‖M-PHASE INDUCER PHOSPHATASE 1‖cell division cycle 25A‖DUAL SPECIFICITY PHOSPHATASE CDC25A‖	functions as a dosage-dependent inducer in mitotic control. it is a tyrosine protein phosphatase required for progression of the cell cycle. it directly dephosphorylates cdc2 and activate its kinase activity. it also dephosphorylates cdk2 in complex with cyclin e, in vitro.

||MMP-12||MME||HME||MMP12||MATRIX METALLOPROTEINASE-12||EC 3.4.24.65||MACROPHAGE METALLOELASTASE PRECURSOR||matrix metalloproteinase 12 preproprotein ||matrix metalloproteinase 12 (macrophage elastase)||	4321	NM_002426	NP_002417	Matrix metalloprotease; degrades elastin	molecular function|zinc binding|P|GO:0008270|Proteome|82269 19//biological process|cell motility|NR|GO:0006928|Proteome|na// molecular function|macrophage elastase|E|GO:0004234|Proteome|822 6919//cellular component|extracellular matrix|NR|GO:0005578|Proteome|na// biological process|proteolysis and peptidolysis|E|GO:0006508|GO:0006928|Proteome|82691 9	role|Protein degradation|NR|Proteome|8226919//organismal role|Cell migration/motility|P|Proteome|7782320//organismal role|Extracellular maintenance|NR|Proteome|8226919//subcellular localization|E cell wall)|NR|Protein cellular (excluding 26919	may be involved in tissue injury and remodeling. has significant elastolytic activity. can accept large and small amino acids at the p1' site, but has a preference for leucine. aromatic or hydrophobic residues are preferred at the p1 site, with small hydrophobic residues (preferably alanine) occupying p3.

||C1S||3.4.21.42||COMPLEMENT COMPONENT 1, s SUBCOMPONENT||COMPLEMENT COMPONENT C1s COMPLEMENT COMPONENT C1s DEFICIENCY||	716	NM_001734	NP_001725	Complement component C1s, a serine protease; contains a cysteine-rich segment	molecular function|serine-type peptidase|P|GO:0008236|Proteome|3500856//molecular function|complement component C1s|E|GO:0003816|Proteome|9856483	biochemical function|Hydrolase|NR|Proteome|3500856//organismal role|Anti-pathogen response|NR|Proteome|9856483//biochemical function|Protease (other than proteasomal)|NR|Proteome|3500856	c1s b chain is a serine protease that combines with c1q and c1s to form c1, the first component of the classical pathway of the complement system. c1r activates c1s so that it can, in turn, activate c2 and c4.

||ESK||PYT||MPS1L1||TTK||EC 2.7.1.-||TTK protein kinase||PHOSPHOTYROSINE-PICKED THREONINE KINASE||ESK, MOUSE, HOMOLOG OF||MONOPOLAR SPINDLE 1-LIKE 1||DUAL SPECIFICITY PROTEIN KINASE TTK||	7272	NM_003318	NP_003309	Dual specificity serine/threonine and tyrosine kinase; similar to S. cerevisiae Mps1p	component|spindle|P|GO:0005819|Proteome|10366450//biological process|oncogenesis|P|GO:0007048|Proteome|1639825//biological process|spindle assembly|P|GO:0007051|Proteome|10366450//biological process|cell cycle control|P|GO:0000074|Proteome|1639825//molecular function|protein tyrosine kinase|E|GO:0004713|Proteome|7737118//biological process|mitot	biochemical function|Transferase|E|Proteome|1639825//organismal role|Control of Cell Proliferation|E|Proteome|1639825	phosphorylates proteins on serine, threonine, and tyrosine. probably associated with cell proliferation.

||RNASEH1|| RNH1||EC 3.1.26.4||ribo nuclease H1||RNASE H1||RIBONU CLEASE H TYPE II||	6040	NM_002936	Ribonuclease H1; binds to double stranded RNA and DNA-RNA hybrids and degrades the RNA strand	molecular function|RNA binding|E|GO :0003723|Pro teome|97995 96//molecular function|ribon uclease|E|G O:0004540|P roteome|979 9596//biologi cal process|RNA catabolism|P| GO:0006401| Proteome|97 99596//molec ular function|nucl eic acid binding|E|GO :0003676|Pro teome|97995 96	role|RNA turnover|P|Pr oteome|9799 596//biochem ical function|Hydr olase|E|Prote ome|9799596 //molecular localization|R NA- associated|P| Proteome|97 99596//bioch emical function|DNA- binding protein|E|Prot eome|979959 6//biochemic al function|RNA- binding protein|E|Prot eome|979959 6//biochemic al function|Nucl ease [endo, exo, ribo, deoxyribo]|E|	this enzyme is an endonucleas e that degrades the rna of rna- dna hybrids specifically.	cytoplasmic (potential).

delta||PRKM13||p38-DELTA||MAPK13||EC 2.7.1.-||STRESS-ACTIVATED PROTEIN KINASE-4||mitogen-activated protein kinase 13||MAP KINASE P38 DELTA||STRESS-ACTIVATED PROTEIN KINASE 4||PROTEIN KINASE, MITOGEN-ACTIVATED, 13||MITOGEN-ACTIVATED PROTEIN KINASE P38 DELTA||protein kinase	5603	NM_002754	NP_002745	MAP kinase 13; activated by stress and proinflammatory cytokines, phosphorylated by MKK6 (PRKMK6)	molecular function|MAP kinase|E|GO:0004707|Proteome|9218798//biological process|stress response|E|GO:0006950|Proteome|9218798//biological process|signal transduction|E|GO:0007165|Proteome|9218798//biological process|antimicrobial humoral response|NR|GO:0006960|Proteome|na	cellular role|Cell stress|NR|Proteome|9218798//biochemical function|Transferase|P|Proteome|9218798//organismal role|Response to injury|P|Proteome|9218798//organismal role|Anti-pathogen response|P|Proteome|9218798	phosphorylates transcription factor atf2.

SMA2||HC3||MU||PSC2||PSC3||PMSA2||EC 3.4.25.1||PROTEASOME COMPONENT . C3||MACROPAIN SUBUNIT C3||PROTEASOME SUBUNIT, ALPHA-TYPE, 2||MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3||PROTEASOME SUBUNIT ALPHA TYPE 2||proteasome (prosome, macropain) subunit,	5683	NM_002787	NP_002778	Alpha subunit 6S-2 of the proteasome (prosome macropain)	cellular component|2 proteasome|P|GO:000583 7|Proteome|811196	cellular role|Protein degradation|NR|Proteome|811196//bio 5653	chemical function|Proteasome subunit|NR|Proteome|2025653	proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity. the component c3 may have a potential regulatory effect on another component(s) of the cytoplasmic and nuclear.

rip5 ||LOC55969|| putative Rab5-interacting protein||	55969	NM_018840					
||MELK||KIAA0175 gene product||likely ortholog of maternal embryonic leucine zipper kinase||	9833	NM_014791	NP_055606				
||pelle||IRAK1||IRAK-1||IRAK||EC 2.7.1.-||Pelle (Drosophila) homolog||interleukin-1 receptor-associated kinase 1||INTERLEUKIN 1 RECEPTOR-ASSOCIATED KINASE 1||	3654	NM_001569	NP_001560	IL-1 receptor-associated kinase 1; associates with IL-1R1 signalling complex, activates NF-kappaB (RELA); has similarity to Pelle	biological process|defense response|NR|GO:0006952|Proteome|na//biological process|signal transduction|P|GO:0007165|Proteome|8599092//biological process|protein phosphorylation|E|GO:0006468|Proteome|8599092//molecular function|NF-kappaB-inducing kinase|P|GO:0004704|Proteome|8599092	biochemical function|Transferase|NR|Proteome|8599092//organismal role|Anti-pathogen response|NR|Proteome|8599092	involved in il-1 pathway. this kinase associates with the il-1 receptor il1-r-1. this association is rapid and il-1 dependent.

PE16||D16S469E||E16||4F2LC||CD98||HLAT1||LAT1||CD98LC||4F2LC||4F2 light chain||CD98 LIGHT CHAIN||INTEGRAL MEMBRANE PROTEIN E16||L-TYPE AMINO ACID TRANSPORTER 1||Solute carrier family 7, member 5||LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBUNIT 1||solute carrier family 7 (cationic amino acid transporter,	8140	NM_003486	NP_003477	Sodium-independent neutral amino acid transporter; helps mediate transport of large and small neutral amino acids; forms a heterodimer with the cell-surface glycoprotein 4F2 heavy chain (MDU1)	cellular component|plasma membrane|NR|GO:0005886|Proteome|na//biological process|amino acid metabolism|E|GO:0006520|Proteome|9751058//biological process|small molecule transport|E|GO:0006832|Proteome|9751058//molecular function|neutral amino acid transporter|E|GO:0015175|Proteome|9751058	cellular role|Amino-acid metabolism|E|Proteome|9751058//biochemical function|Active transporter, secondary|E|Proteome|9751058	sodium-independent, high-affinity transport of large neutral amino acids. involved in cellular amino acid uptake.	integral membrane protein (probable).

||MAC30||hypothetical protein||	27346	L19183	||CCNB2||G2/MITOTIC-SPECIFIC CYCLIN B2||	9133	NM_004701	NP_004692	Cyclin B2; member of the cyclin family of CDK kinase regulatory subunits
||C1orf2||CHROMOSOME 1 OPEN READING FRAME 2||	10712	NM_006589	NP_006580	essential for the control of the cell cycle at the g2/m (mitosis) transition.

AKR1C2||MC								process|dige	
DR2||DD/BA								stion|P|GO:0	
BP||HAKRD||								007586|Prote	
DDH2||EC								ome|8573067	
1.3.1.20||ALD								//biological	
O-KETO								process|lipid	
REDUCTAS								metabolism|E	
E								|GO:0006629	
D||PROBABL								|Proteome|85	
E TRANS-1,2-								73067//biolog	
DIHYDROBE								ical	
NZENE-1,2-								process|bile	
DIOL								acid	
DEHYDROG								transport|P|G	
ENASE||3-								O:0015721|P	
@ALPHA-						Aldo-keto		roteome|857	
HYDROXYS						reductase		3067//molecu	
TEROID						1C2;		lar	
DEHYDROG						converts		function|elect	
ENASE,						dihydrotestos		ron	biochemical
TYPE						terone to 5 a-		transporter|E|	function|Oxid
III||CHLORD						androstane-3		GO:0005489|	oreductase|E|
ECONE						a, 17 b-diol;		Proteome|84	Proteome|84
REDUCTAS						binds bile,		86699//molec	86699//bioch
E						possibly		ular	emical
HOMOLOG						functions in		function|bile	function|Smal
HAKRD||DIH						intracellular		acid	l molecule-
YDRODIOL						bile transport		transporter|P|	binding
DEHYDROG						and		GO:0015125|	protein|E|Prot
ENASE/BILE						xenobiotic		Proteome|85	eome|857306
ACID-						metabolism		73067//biolog	7
	1646	NM_001354	NP_001345						

cytoplasmic (potential).

					process|onco genesis|P|G O:0007048|P roteome|927 8511\//biologi cal process|gam etogenesis|P| GO:0007276| Proteome|93 82850\//molec ular function|prote in kinase|E|GO: 0004672|Prot eome|927851 1\//molecular function|tumo r suppressor|P| GO:0008181| Proteome|93 82850\//cellul ar component|m eiotic chromosome| E|GO:000571 1|Proteome|9 382850\//biolo	involved in cell cycle arrest when dna damage has occurred or when unligated dna is present. binds to and phosphorylat es cdc25a, cdc25b and cdc25c. phosphorylati on of cdc25c creates a binding site for 14-3-3 protein which inhibits cdc25c. this prevents activation of the cdc2-cyclin b complex and prevents mitotic entry. phosphorylat es cdc25c on serine-216. nuclear.
1111	NM_001274	NP_001265	Protein kinase; inhibits mitotic entry after DNA damage, required for the DNA damage checkpoint; strongly similar to murine Chek1	||| ||CHEK1||CH K1||EC 2.7.1.-||SERINE/TH REONINE-PROTEIN KINASE CHK1||CHK1 (checkpoint, S.pombe) homolog||Ch eckpoint, S. pombe, homolog of, 1||	

||FLJ23378||hypothetical protein MGC5487||	79071	NM_024090	NP_076995	||COCH-5B2||COCH||DFNA31||COCH5B2||DFNA9||cochlin precursor||deafness, autosomal dominant 31||coagulation factor C (Limulus polyphemus) homology (cochlin)||coagulation factor C (Limulus polyphemus homolog); cochlin||	1690	NM_004086	NP_004077	Expressed in inner ear structures	biological process|hearing|EI|GO:0007605|Proteome|9806553	secreted (potential).

||hypothetical protein FLJ11011||	55284	NM_018299	NP_060769	Member of the ubiquitin-conjugating enzyme (E2) family			
||HHGP||HHGP protein||	56952	NM_020200	NP_064585				
1||ABCA1||TD||TGD||CERP||HDLDT1||ABC1||ABC TRANSPORTER 1||ATP-binding cassette 1||cholesterol efflux regulatory protein||ATP-BINDING CASSETTE TRANSPORTER 1||ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1||ATP-binding cassette, sub-family A member 1||ATP-BINDING CASSETTE, SUBFAMILY A, MEMBER 1||high	19	NM_005502	NP_005493	ATP binding cassette transporter A1; anion transporter required for engulfment of apoptotic cells, may also have a role in intracellular cholesterol transport	component|membrane fraction|P|GO:0005624|Proteome|10431236//molecular function|anion transporter|E|GO:0008509|Proteome|9006906//molecular function|sterol transporter|P|GO:0015248|Proteome|10431236//biological process|cholesterol metabolism|P|GO:0008203|Proteome|10431236//molecular function|adenosinetriphosphatase|P|GO:	function|Hydrolase|P|Proteome|10431236//organismal role|Intercellular transport|E|Proteome|10431236//molecular localization|Integral membrane|P|Proteome|10431236//biochemical function|ATP-binding cassette|NR|Proteome|10431236//subcellular localization|Unspecified membrane|P|Proteome|10431236//biochemical function|Active transporter, primary|P|Pro	camp-dependent and sulfonylurea-sensitive anion transporter. key gatekeeper influencing intracellular cholesterol transport.

||ID-GAP||RACGAP1||MGCRACGAP||GTPase-ACTIVATING PROTEIN, RAC, 1||RAC GTPase-ACTIVATING PROTEIN 1||Rac GTPase activating protein 1||RAC GTPase-ACTIVATING PROTEIN, MALE GERM CELL||	29127	NM_013277	NP_037409	Strong similar to murine Racgap1 GTPase-activating protein for rac
||RAB10||ras-related GTP-binding protein||RAS-RELATED PROTEIN RAB-10||RAB10, member RAS oncogene family||	10890	NM_016131	NP_057215	
				may be involved in vesicular trafficking and neurotransmitter release.

||RAP2B||RAS-RELATED PROTEIN RAP-2B||RAS-RELATED PROTEIN 2B||RAP2B, member of RAS oncogene family||	5912	AL713766	NP_002877	Member of the ras family of GTP binding proteins	molecular function|GTP binding|E|GO:0005525|Proteome|21186 48//biological process|sign al transduction| PIGO:000716 5|Proteome|2 118648	biochemical function|Hydrolase|E|Proteome|2118648 //biochemical function|GTP-binding protein/GTPase|E|Proteome|2118648
||CCNB1||CCNB||G2/mitotic-specific cyclin B1||	891	NM_031966	NP_114172				essential for the control of the cell cycle at the g2/m (mitosis) transition.

||desmocollin-3||DGII/IIII||DSC2||DSC3||DG2||DG2/3||CDHF2||DSC3, FORMERLY||DESMOCOLLIN 2A/2B PRECURSOR||DESMOCOLLIN 3, FORMERLY||desmosomal glycoprotein II/IIII||DESMOSOMAL GLYCOPROTEIN II AND IIII||desmocollin 2, isoform Dsc2b preproprotein ||desmocollin 2, isoform Dsc2a preproprotein ||	1824	NM_004949	NP_077740	Desmocollin 2; related to cadherin glycoproteins found in desmosomes	biological process|cell adhesion|P|GO:0007155|Proteome|203 7591//molecular function|cell adhesion|P|GO:0005194|Proteome|203	7591//cellular componentlin tercellular junction|NR|GO:0005911| Proteome|na	biochemical function|Adhesin/agglutinin| P|Proteome|2 037591//subcellular localization|cell junction|NR|Proteome|203 7591	component of intercellular desmosome junctions. involved in the interaction of plaque proteins and intermediate filaments mediating cell cell adhesion. may contribute to epidermal cell positioning (stratification) by mediating differential adhesiveness between cells that express type i different membrane isoforms. protein.

||MDC9||MCMP||KIAA0021||ADAM9||MLTNG||MYELOMA CELL METALLOPROTEINASE||METALLOPROTEINASE-LIKE, DISINTEGRIN-LIKE, AND CYSTEINE-RICH PROTEIN 9||a disintegrin and metalloproteinase domain 9 preproprotein||a disintegrin and metalloproteinase domain 9 (meltrin gamma)||	8754	NM_003816	NP_003807	Member of ADAM family of zinc metalloproteases; related ADAM family members contain disintegrin domains	molecular function|integrin ligand|P|GO:0005178|Proteome|8647900//molecular function|metallopeptidase|P|GO:0008237|Proteome|8647900//biological process|protein kinase cascade|P|GO:0007243|Proteome|8647900//cellular component|integral plasma membrane protein|E|GO:0005887|Proteome|8647900	biochemical function|Hydrolase|NR|Proteome|8647900//molecular localization|Integral membrane|P|Proteome|8647900//biochemical function|Protease (other than proteasomal)|NR|Proteome|8647900

							component|endoplasmic reticulum|E|GO:0005783|Proteome|8050590//molecular function|signal sequence receptor|E|GO:0005048|Proteome|8050590//cellular component|integral membrane protein|E|GO:0016021|Proteome|8050590//biological process|co-translational membrane targeting|E|GO:0006613|Proteome|8050590//biological process|positive control of cell	cellular role|Protein translocation| translocation|NR|Proteome|8050590//molecular localization|integral membrane|NR|Proteome|8050590	are part of a complex whose function is to bind ca(2+) to the er membrane and thereby regulate the retention of er resident proteins. may be involved in the recycling of the translocation apparatus after completion of the translocation process or may function as a membrane-bound chaperone facilitating folding of translocated proteins.	type i membrane protein. endoplasmic reticulum.
‖SSR1‖TRAP-ALPHA‖SSR-ALPHA‖TRAPA‖TRAP alpha‖TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR‖SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT‖signal sequence receptor, alpha (translocon-associated protein alpha)‖	6745	NM_003144	NP_003135	Signal sequence receptor alpha (translocon-associated protein alpha)					

‖ERO1L‖ERO1 (S. cerevisiae)-like‖	30001	NM_014584	NP_055399	May be required for formation of disulfide bonds in ER protein folding	component|microsome|E|GO:0005792|Proteome|10671517//biological process|protein folding|P|GO:0006457|Proteome|10671517//cellular component|membrane fraction|E|GO:0005624|Proteome|10671517//biological process|protein modification|E|GO:0006464|Proteome|10671517//biological process|temperature response|E|GO:0009266|Proteome|10671517	biochemical function|Oxidoreductase|P|Proteome|10671517//molecular localization|Integral membrane|E|Proteome|10671517//subcellular localization|Unspecified membrane|E|Proteome|10671517
‖AURORA2‖BTAK‖ARK1‖STK15‖AURORA-RELATED KINASE 1‖serine/threonine kinase 15‖Serine/threonine protein kinase 15‖	8465	AF011468		Centrosome-associated serine/threonine kinase	biological process|mitosis|P|GO:0007067|Proteome|9153231//biological process|oncogenesis|E|GO:0007048|Proteome|9771714//molecular function|protein kinase|E|GO:0004672|Proteome|9153231//cellular component|spindle pole body|E|GO:0005816|Proteome|9153231//biological process|protein phosphorylation|E|GO:0006468|Proteome|9153231	biochemical function|Transferase|P|Proteome|9153231//subcellular localization|Nuclear|E|Proteome|9771714

								‖HP1HS-GAMMA‖HECH‖HP1-GAMMA‖GAMMA‖CBX3‖heterochromatin-like protein 1‖MODIFIER 2 PROTEIN‖heterochromatin protein HP1 gamma‖HP1, DROSOPHILA, HOMOLOG OF‖CHROMOBOX PROTEIN HOMOLOG 3‖HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA‖chromobox homolog 3 (Drosophila HP1 gamma)‖
11335	NM_016587	NP_057671	Similar to Drosophila HP1; interacts with lamin B receptor, implicated in heterochromatin association with inner nuclear membrane	cellular component|nucleus|P|GO:0005634|Proteome|8663349//molecular function|chromatin binding|P|GO:0003682|Proteome|8663349	subcellular localization|Nuclear|P|Proteome|8663349//biochemical function|DNA-binding protein|P|Proteome|8663349//cellular role|Chromatin/chromosome structure|P|Proteome|8663349//molecular localization|DNA-associated (direct or indirect)|P|Proteome|8663349	component of heterochromatin. may interact with lamin b receptor (lbr). this interaction can contribute to the association of the heterochromatin with the inner nuclear membrane.	nuclear (potential).	‖HSPC121‖BIND1‖hypothetical protein; butyrate-induced transcript 1‖
51495	AK027421	NP_057479	Protein induced by sodium butyrate treatment; acts downstream of the monomeric GTPase RAC1	molecular function|GTPase activator|E|GO:0005096|Proteome|10747961//biological process|activation of JUN kinase|E|GO:0007257|Proteome|10747961//biological process|NIK-I-kappaB/NF-kappaB cascade|E|GO:0007249|Proteome|10747961//biological process|small GTPase mediated signal transduction|E|GO:0007264|Proteome|10747961				

‖NMU‖NMU-25‖NEUROMEDIN U-25 PRECURSOR‖	10874	NM_006681	NP_006672	Neuromedin U; similar to rat NmU	function|ligand|E|GO:0005102|Proteome|10811630//biological process|digestion|P|GO:0007586|Proteome|7619205//biological process|signal transduction|P|GO:0007165|Proteome|7619205//biological process|smooth muscle contraction regulation|P|GO:0006940|Proteome|7619205//biological process|G-protein linked receptor protein signalling pathway|E|G	organismal role|Muscle action|P|Proteome|7619205//molecular localization|Soluble|E|Proteome|10811630//organismal role|Cell-to-cell signalling|P|Proteome|7619205//subcellular localization|Extracellular (excluding cell wall)|P|Proteome|7619205	stimulates muscle contractions of specific regions of the gastrointestinal tract. in humans, nmu stimulates contractions of the ileum and urinary bladder.	secreted.
	115908	NM_138455	NP_612464					
‖hypothetical protein PRO1855‖	55379	NM_018509	NP_060979					
‖hypothetical protein FLJ20151‖	54837	NM_017689	NP_060159					
‖hypothetical protein FLJ10493‖	55151	NM_018112	NP_060582					

||RNF24||G1L ||ring finger protein 24||goliath-like protein (C3HC4 type)||	11237	NM_007219	NP_009150	Region of low similarity to a region of murine sperizin ; may mediate protein-protein interactions; contains a C3HC4 type (RING) zinc finger	
||KIAA0042 gene product||	9928	NM_014875	NP_055690		
3||IMMUNOGLOBULIN Gm3||HEAVY CHAIN DISEASE PROTEIN||IG GAMMA-3 CHAIN C REGION||immunoglobulin gamma 3 (Gm marker)||Immunoglobin heavy constant gamma 3 (G3m marker)||Constant region of heavy chain of IgG3||immunoglobulin heavy constant gamma 3 (G3m marker)||immunoglobulin heavy	3502	BC019046			
||RALA||RAL||RAS-RELATED PROTEIN RAL-A||v-ral simian leukemia viral oncogene homolog A (ras related)||RAS-like protein A; Simian leukemia viral (v-ral) oncogene homolog||	5898	NM_005402	NP_005393	Member of the ras family of GTP binding proteins, A	biological process|chemotaxis|E|GO:0006935|Proteome|10848592//molecular function|GTP binding|E|GO:0005525|Proteome|2550440//molecular function|protein binding|E|GO:0005515|Proteome|10848592//biological process|signal transduction|P|GO:0007165|Proteome|10848592 biochemical function|Hydrolase|E|Proteome|2550440//organismal role|Cell migration/motility|E|Proteome|10848592//biochemical function|GTP-binding protein/GTPase|E|Proteome|2550440

||FSP-2||fibrousheathin II||	26256	NM_012189	NP_036321	Low similarity to murine Sp17		
||PPAT||GPAT||ATASE||AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR||EC 2.4.2.14||GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE||phosphoribosyl pyrophosphate amidotransferase||	5471	NM_002703	NP_002694	Phosphoribosyl pyrophosphate (PRPP) amidotransferase; transfers amine group from Gln to PRPP to form 5-phosphoribosylamine	biological process|purine nucleotide biosynthesis|E|GO:0006164|Proteome|8106516//molecular function|amidophosphoribosyltransferase|E|GO:0004044|Proteome|8106516	biochemical function|Transferase|E|Proteome|8106516

||FLJ13784||hypothetical protein MGC3067||	79139	AK023846	NP_077271		uk3	
||WWP1||AIP5||hypothetical protein DKFZp434D2111||WW domain-containing protein 1||	11059	NM_007013	NP_008944	WW domain-containing protein 1; may be involved in protein-protein interactions; contains a HECT domain found in ubiquitin ligases	molecular function|ubiquitin--protein ligase|P|GO:0004842|Proteome|9647693	
||FZD10||frizzled (Drosophila) homolog 10||FRIZZLED, DROSOPHILA, HOMOLOG OF, 10||	11211	NM_007197	NP_009128	Frizzled-10; G protein-coupled receptor; similar to the frizzled family of receptors	cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|10448064//molecular function|frizzled receptor ligand receptor|P|GO:0004928|Proteome|10448064//biological process|frizzled receptor signalling pathway|P|GO:0007222|Proteome|10448064	organismal role|Other development|P|Proteome|10448064//organismal role|Cell fate specification|P|Proteome|10448064//molecular localization|Integral membrane|P|Proteome|10448064//biochemical function|Receptor (signalling)|P|Proteome|10448064

||hypothetical protein FLJ11273||	54664	NM_018374	NP_060844				
||PRKMK1||MAPKK1||MEK1||MAP2K1||MKK1||EC 2.7.1.- ||MAPKK 1||MAPK/ERK KINASE 1||ERK ACTIVATOR KINASE 1||DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1||protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)||	5604	NM_002755	NP_002746	MAP kinase kinase 1; activates the MAP kinase ERK1 (PRKM3)	biological process|chemotaxis|E|GO:0006935|Proteome|10570282//biological process|cell motility|E|GO:0006928|Proteome|10912793//molecular function|protein kinase|E|GO:0004672|Proteome|10570282//molecular function|MAP kinase kinase|E|GO:0004708|Proteome|8388392//biological process|signal transduction|E|GO:0007165|Proteome|10570282	biochemical function|Transferase|E|Proteome|10570282//organismal role|Cell migration/motility|E|Proteome|10912793	catalyzes the concomitant phosphorylation of a threonine and a tyrosine residue in a thr-glu-tyr sequence located in map kinases. activates erk1 and erk2 map kinases.

UBR1||BUB1B||Bub1A||MAD3L||EC 2.7.1.-||MAD3/BUB1-RELATED PROTEIN KINASE||MITOTIC CHECKPOINT GENE BUB1B||MITOTIC CHECKPOINT KINASE MAD3L||MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINASE BUB1 BETA||BUB1, S. CEREVISIAE, HOMOLOG OF, BETA||budding uninhibited	701	NM_001211	NP_001202	Protein kinase; required for mitotic spindle checkpoint and normal mitotic progression	component|a process|mitosis|E|GO:0007067|Proteome|10477750//cellular component|kinetochore|E|GO:0005699|Proteome|9660858//molecular function|protein kinase|E|GO:0004672|Proteome|10477750//biological process|cell proliferation|P|GO:0008283|Proteome|10477750//biological process|mitotic checkpoint|E|GO:0007093|Proteome|10477750//cellular	biochemical function|Transferase|E|Proteome|10477750//subcellular localization|Nuclear|E|Proteome|10477750//organismal role|Control of Cell Proliferation|P|Proteome|10477750	probable component of the mitotic checkpoint that delays anaphase until all chromosomes are properly attached to the mitotic spindle. can interact with bub3, cenp-f, cenp-e and mitosin.	cytoplasmic in interphase cells. bound to bub3 or cenp-e, it can be localized to nuclear kinetochores.

||p55||PSMD12||PROTEASOME 26S SUBUNIT, NON-ATPase, 12||proteasome (prosome, macropain) 26S subunit, non-ATPase, 12||	5718	NM_002816	NP_002807	Non-ATPase subunit of the 26S proteasome (prosome macropain)	cellular component|26S proteasome|E|GO:0005837|Proteome|8811196//cellular component|19S proteasome regulatory particle|P|GO:0005838|Proteome|9426256	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|9426256		
||HSPC150 protein similar to ubiquitin-conjugating enzyme||	29089	NM_014176	NP_054895					
||PROAM-N20||preproadrenomedullin||AM||PAMP||ADM||ADM PRECURSOR||PROAM N-TERMINAL 20 PEPTIDE||PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE||	133	NM_001124	NP_001115	Precursor of adrenomedullin (AM) and the putative 20 amino acid peptide proAM-N20; regulates blood pressure and heart rate	function|ligand|P|GO:0005102|Proteome|8524787//biological process|pregnancy|P|GO:0007565|Proteome|10822232//biological process|excretion|NR|GO:0007588|Proteome|na//biological process|circulation|P|GO:0008015|Proteome|8074714//cellular component|soluble fraction|E|GO:0005625|Proteome|10822232//biological process|cAMP biosynthesis|P|GO:000617	molecular localization|Soluble|E|Proteome|10822232//organismal role|Cell-to-cell signalling|P|Proteome|8074714//organismal role|Osmoregulation and Excretion|E|Proteome|10867102	pamp are potent hypotensive and vasodilatator agents. numerous actions have been reported most related to the physiologic control of fluid and electrolyte homeostasis. in the kidney, am is diuretic and natriuretic, and both am and pamp inhibit aldosterone secretion by direct adrenal actions. in pituitary gland, both peptides at	secreted.

‖LOC51026‖ CGI-141 protein‖	51026	NM_016072	NP_057156				
‖PRSS24‖STEAP‖SIX-TRANSMEMBRANE EPITHELIAL ANTIGEN OF THE PROSTATE‖six transmembrane epithelial antigen of the prostate (NOTE: non-standard symbol and name)‖	26872	NM_012449	NP_036581	Six transmembrane epithelial antigen of the prostate; prostate-specific cell-surface antigen	function|transporter|P|GO:0005215|Proteome|10588738//molecular function|tumor antigen|E|GO:0008222|Proteome|10588738//cellular component|plasma membrane|E|GO:0005886|Proteome|10588738//cellular component|intercellular junction|E|GO:0005911|Proteome|10588738//molecular function|channel/pore class transporter|P|GO:0015267|Proteome|10	molecular localization|Integral membrane|P|Proteome|10588738	
‖RY1‖putative nucleic acid binding protein RY-1‖	11017	BC017890					molecular function|DNA binding|P|GO:0003677|Proteome|7931148

||XCT||SLC7A11||cystine/glutamate transporter||solute carrier family 7, (cationic amino acid transporter, y+ system) member 11||	23657	NM_014331	NP_055146	Strongly similar to murine Xct; may act as an amino acid transporter	biological process|protein complex assembly|NR|GO:0006461|Proteome|na//cellular component|integral membrane protein|P|GO:0016021|Proteome|10206947//molecular function|cystine/glutamate antiporter|P|GO:0015327|Proteome|10206947			
||CDC25||EC 3.1.3.48||phosphotyrosine phosphatase||mitosis inducer CDC25||m-phase inducer phosphatase 3||dual specificity phosphatase CDC25C||cell division cycle 25C protein, isoform a||cell division cycle 25C protein, isoform b||	995	NM_001790	NP_073720	Protein tyrosine phosphatase; dephosphorylates cyclin B-bound CDC2 and triggers entry into mitosis	biological process|cell proliferation|P|GO:0008283|Proteome|1828290//biological process|control of mitosis|E|GO:0007088|Proteome|1828290//biological process|mitotic start control point|P|GO:0007089|Proteome|2195549	organismal role|Control of Cell Proliferation|P|Proteome|1828290	functions as a dosage-dependent inducer in mitotic control. it is a tyrosine protein phosphatase required for progression of the cell cycle. it directly dephosphorylates cdc2 and activate its kinase activity.	nuclear.

||MD2||MD-2||MD2 PROTEIN||MD-2 protein||	23643	NM_015364	NP_056179	Subunit of a receptor complex for lipopolysaccharide (LPS); may function as a link between TLR4 and LPS signaling	process|cellular defense response|P|GO:0006968|Proteome|10359581|biological process|antibacterial humoral response|P|GO:0006961|Proteome|10359581|biological process|antibacterial humoral response|NR|Proteome|10359581	function|core ceptor|E|GO:0015026|Proteome|10359581|cellular component|plasma membrane|E|GO:0005886|Proteome|10359581|biological process|cellular defense response|P|GO:0006968|Proteome|10359581|biological process|antibacterial humoral response|P|GO:0006961|Proteome|10359581|biological process|antibacterial humoral response|NR|Proteome|10359581	function|Receptor (signalling)|E|Proteome|10359581			

component|c onnexon|E|G O:0005922|P roteome|185 0831//molecu lar function|ion transporter|E| GO:0015075| Proteome|16 96265//molec ular function|conn exon channel|E|G O:0015285|P roteome|185 0831//biologi cal process|heart development| Connexin 43, a cardiac gap junction protein; may act in synchronizing heart contraction and embryonic development	role|Muscle action|P|Prot eome|771564 0//organismal role|Embryoni c develop ment| E|Proteome|7 715640//subc ellular localization|C ell junction|P|Pr oteome|1696 265//organis mal role|Intercellu lar transport|P|Pr oteome|1696 265//molecul ar localization|In tegral membrane|N R|Proteome|1 850831//bioc hemical function|Cha nnel [passive transporter]|E	one gap junction consists of a cluster of closely packed pairs of transmembra ne channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	integral membrane protein.	NP_000156	NM_000165	2697
||GJA1||CX43 ||HEART CONNEXIN|| GAP JUNCTION PROTEIN, ALPHA-1||GAP JUNCTION PROTEIN, 43-KD||GAP JUNCTION ALPHA-1 PROTEIN||G AP JUNCTION 43 KDA HEART PROTEIN||ga p junction protein, alpha 1, 43kD (connexin 43)||						

||CPE||CPH|| EC 3.4.17.10||ENKEPHALIN CONVERTASE||carboxypeptidase E precursor||CARBOXYPEPTIDASE H PRECURSOR||PROHORMONE PROCESSING CARBOXYPEPTIDASE||	1363	NM_001873	NP_001864	Carboxypeptidase E; metalloprotease that has a role in processing neuropeptides; Strongly similar to murine Cpe	process|metabolism|E|GO:0008152|Proteome|7663508//cellular component|plasma membrane|E|GO:0005886|Proteome|9019408//molecular function|carboxypeptidase|E|GO:0004180|Proteome|9019408//biological process|protein modification|NR|GO:0006464|Proteome|na//biological process|proteolysis and peptidolysis|NR|GO:0006508|Proteome|na//biologic	molecular localization|Soluble|E|Proteome|2334405//organismal role|Control of body size|P|Proteome|7663508//organismal role|Cell-to-cell signalling|NR|Proteome|2334405//subcellular localization|Unspecified membrane|NR|Proteome|2334405	removes residual c-terminal arg or lys remaining after initial endoprotease cleavage during prohormone processing.	secretory granules of pancreatic islets, adrenal gland, pituitary and brain.

isoform||EC 3.1.3.48||EC 3.1.3.2||Bf isoform||PHOSPHATASE, ACID, OF ERYTHROCYTE||acid phosphatase 1, soluble||acid phosphatase 1 isoform a||acid phosphatase 1 isoform b||ADIPOCYTE ACID PHOSPHATASE, ISOZYME ALPHA||LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE||RED CELL ACID PHOSPHAT	52	NM_004300	NP_009030	Phosphotyrosyl protein phosphatase (acid phosphatase 1)	cellular component|cytoplasm|NR|GO:0005737|Proteome|na//cellular component|soluble fraction|E|GO:0005625|Proteome|1587862//molecular function|acid phosphatase|E|GO:0003993|Proteome|1587862	biochemical function|Hydrolase|E|Proteome|1587862//molecular localization|Soluble|E|Proteome|1587862//subcellular localization|Cytoplasmic|NR|Proteome|1587862//biochemical function|Other phosphatase|E|Proteome|1587862	acts on tyrosine phosphorylated proteins, low-mw aryl phosphates and natural and synthetic acyl phosphates.	cytoplasmic.

3-ALPHA||MIP-3a||SCYA20||CCL20||MIP3A||EXODUS 1||BETA CHEMOKINE EXODUS-1||CC CHEMOKINE LARC||LIVER AND ACTIVATION-REGULATED CHEMOKINE ||MACROPHAGE INFLAMMATORY PROTEIN 3-ALPHA||CC CHEMOKINE LIGAND 20||MACROPHAGE INFLAMMATORY PROTEIN 3 ALPHA||SMALL	6364	NM_004591	NP_004582	Cytokine A20 (exodus); chemotactic factor for lymphocytes, but not a chemotactic factor for monocytes	function|chemokine|GO:0008009|Pro teome|10438 902//biological process|chemotaxis|GO:0006935|Proteome|104 38902//biological process|immune response|GO:0006955|Proteome|105 21347//biological process|signal transduction| GO:000716 5|Proteome|9 038201//cellular component|extracellular space|GO: 0005615|Proteome|903820 1	organismal role|Response to injury|Proteome|90938201 //organismal role|Anti-pathogen response|Proteome|903 8201//organismal role|Cell migration/motility|Proteome|10521347 //organismal role|Cell-to-cell signalling|NR| Proteome|90 38201//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|903820 1	chemotactic factor that attracts lymphocytes and, slightly, neutrophils, but not monocytes. inhibits proliferation of myeloid progenitors in colony formation assays. may be involved in formation and function of the mucosal lymphoid tissues by attracting lymphocytes and dendritic cells towards epithelial cells. binds to ccr6. secreted.

||CROC1||UEV1||CROC-1||UEV1A||CIR1||UEV-1||UBE2V1||DNA-binding protein||ubiquitin-conjugating enzyme E2 variant 1, isoform a||ubiquitin-conjugating enzyme E2 variant 1, isoform c||ubiquitin-conjugating enzyme E2 variant 1, isoform b||	7335	AL110132	NP_071887	Ubiquitin-conjugating E2 enzyme variant 1; may play a role in signaling for DNA repair; member of an E2 subfamily	biological process|cell cycle control|E|GO:0000074|Proteome|9418904//biological process|polyubiquitylation|E|GO:0000209|Proteome|10089880//biological process|DNA repair regulation|P|GO:0006282|Proteome|10089880//molecular function|ubiquitin conjugating enzyme|E|GO:0004840|Proteome|10089880		
||COL4A2||COLLAGEN, TYPE IV, ALPHA-2||collagen, type IV, alpha 2||COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR||COLLAGEN OF BASEMENT MEMBRANE, ALPHA-2 CHAIN||	1284	NM_001846	NP_001837	Alpha 2 subunit of type IV collagen; may be an extracellular matrix protein that forms basement membranes; member of a subfamily of collagen extracellular matrix proteins	molecular function|collagen|NR|GO:0005202|Proteome|na//cellular component|collagen type IV|NR|GO:0005587|Proteome|na	role|Extracellular matrix component|NR|Proteome|3025878//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|3025878//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|3025878//subcellular localization|Basement membrane (extracellular matrix)|NR|Proteome|3025878//subcellular localization|Extracellular	type iv collagen is the major structural component of glomerular basement membranes (gbm), forming a 'chicken-wire' meshwork together with laminins, proteoglycans and entactin/nidogen.

||SNN||Stannin||AG8_1||	8303	NM_003498	NP_003489	Stannin; may play a role in the toxicity of organotins	biological process|stress response|P|GO:0006950|Proteome|9657854//biological process|response to abiotic stimulus|P|GO:0009628|Proteome|9657854	plays a role in the toxic effects of organotins.
||TGT||USP14||QUEUINE TRNA-RIBOSYLTRANSFERASE ||EC 2.4.2.29||GUANINE INSERTION ENZYME||ubiquitin specific protease 14 (tRNA-guanine transglycosylase)||	9097	NM_005151	NP_005142	Similar to ubiquitin-specific cysteine (thiol) proteases and tRNA-guanine transglycosylase; may cleave ubiquitin from ubiquitin-conjugated proteins	biological process|deubiquitylation|E|GO:0006514|Proteome|9827704//molecular function|tRNA guanylyltransferase|P|GO:0008193|Proteome|8579355//molecular function|cysteine-type endopeptidase|E|GO:0004197|Proteome|9827704//molecular function|ubiquitin-specific protease|P|GO:0004843|Proteome|8579355	

||3.6.1.37||ATP1B3||ATPB-3||Na,K-ATPase BETA-3 POLYPEPTIDE||SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN||SODIUM/POTASSIUM-DEPENDENT ATPASE BETA-3 SUBUNIT||ATPase, Na+/K+ TRANSPORTING, BETA-3 POLYPEPTIDE||ATPase, Na+/K+ transporting, beta 3 polypeptide||	483	NM_001679	NP_001670	Beta 3 subunit of the Na+/K+ -ATPase	biological process|small molecule transport|P|GO:0006832|Proteome|8798450//molecular function|sodium/potassium-exchanging ATPase|P|GO:0005391|Proteome|8798450//cellular component|sodium/potassium-transporting ATPase|P|GO:0005890|Proteome|8798450	molecular localization|Integral membrane|P|Proteome|8798450//subcellular localization|Unspecified membrane|P|Proteome|8798450	this is the non-catalytic component of the active enzyme, which catalyzes the hydrolysis of atp coupled with the exchange of na and k ions across the plasma membrane. the exact function of this glycoprotein is not known.	type ii membrane protein.

||MCM2||MCM7||P1.1-MCM3||CDC47||MCM2, FORMERLY|| CDC47 HOMOLOG|| CDC47, S. CEREVISIAE , HOMOLOG OF||DNA REPLICATION LICENSING FACTOR MCM7||minichromosome maintenance deficient (S. cerevisiae) 7||MINICHROMOSOME MAINTENANCE, S. CEREVISIAE , HOMOLOG OF, 7||	4176	NM_005916	NP_005907	Member of the MCM family; chromatin-binding protein, has a probable role in DNA replication	cellular component|chromatin|P|GO:0005717|Proteome|879 8650||biological process|DNA replication|P|GO:0006260|Proteome|8798650	cellular role|DNA synthesis|P|replication and cell proliferation.	acts as a factor that allows the dna to undergo a single round of replication per cell cycle. required for dna	nuclear (by similarity).

cellular component|nucleus|E|GO:0005634|Proteome|875136|biological process|DNA replication|P|GO:0006260|Proteome|87 51386//biolog	||MCM5||P1-CDC46||CDC46||CDC46 HOMOLOG|| DNA REPLICATION LICENSING FACTOR MCM5||minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46)||	4174	NM_006739	NP_006730	Similar to S. cerevisiae CDC46 which is involved in the initiation of DNA synthesis; member of the MCM family of chromatin-binding proteins	ical process|cell cycle control|P|GO:0000074|Proteome|922343 7//molecular function|cell cycle regulator|P|GO:0003750|Proteome|922 3437	cellular role|DNA synthesis|P|Proteome|875 1386//subcellular localization|Nuclear|E|Proteome|875136 6	nuclear.

||URK||UPA|| PLAU||EC 3.4.21.73||U-PLASMINOGEN ACTIVATOR||PLASMINOGEN ACTIVATOR, URINARY||plasminogen activator, urokinase||UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR||	5328	NM_002658	NP_002649	Urokinase plasminogen activator; serine protease that cleaves plasminogen to form plasmin	process|chemotaxis|E|GO:0006935|Proteome|10749881//molecular function|cell adhesion|NR|GO:0005194|Proteome|na//biological process|blood coagulation|NR|GO:0007596|Proteome|na//biological process|signal transduction|E|GO:0007165|Proteome|10749881//cellular component|extracellular space|NR|GO:0005615|Proteome|na//molecular function|U-	organismal role|Blood clotting|NR|Proteome|6589620//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|6589620	potent plasminogen activator and is clinically used for therapy of thrombolytic disorders.

||MIG||SCYB9 ||chemokine|| CMK||monokine induced by gamma interferon||SMALL INDUCIBLE CYTOKINE SUBFAMILY B, MEMBER 9||	4283	NM_002416	NP_002407	Member of the chemokine family of cytokines	function|cytokine|P|GO:0005125|Proteome|2115167//molecular function|chemokine|E|GO:0008009|Proteome|10903763//biological process|chemotaxis|E|GO:0006935|Proteome|10903763//biological process|defense response|P|GO:0006952|Proteome|2115167//biological process|immune response|NR|GO:0006955|Proteome|na//biological process|sign	organismal role|Cell migration/motility|E|Proteome|10903763//organismal role|Cell-to-cell signalling|NR|Proteome|8476424//subcellular localization|Extracellular (excluding cell wall)|P|Proteome|8476424		
||IBP3||IGFBP3||IBP-3||IGFBP-3||IGF-BINDING PROTEIN 3||INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN 3||INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR||	3486	NM_000598	NP_000589	Member of the insulin-like growth factor binding family of proteins; may bind to and modulate insulin-like growth factor activity	biological process|signal transduction|P|GO:0007165|Proteome|10766744//cellular component|extracellular space|NR|GO:0005615|Proteome|na//molecular function|insulin-like growth factor receptor binding protein|E|GO:0005067|Proteome|10766744	organismal role|Cell migration/motility|E|Proteome|10766744//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|1373120	igf-binding proteins prolong the half-life of the igfs and have been shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptors.	secreted.

||GCSH||GCE||NKH||GLYCINE CLEAVAGE SYSTEM H PROTEIN, MITOCHONDRIAL PRECURSOR||glycine cleavage system protein H (aminomethyl carrier)||	2653	NM_004483	NP_004474	H-protein; glycine cleavage system component, transfers methylamine group of glycine from P protein to T protein	cellular component|mitochondrion|P|GO:0005739|Proteome|3348809//biological process|glycine catabolism|P|GO:0006546|Proteome|1671321//molecular function|aminomethyltransferase|P|GO:0004047|Proteome|3348809//cellular component|glycine cleavage system|P|GO:0005960|Proteome|3348809	biochemical function|Transferase|P|Proteome|3348809//cellular role|Amino-acid metabolism|P|Proteome|3348809//subcellular localization|Mitochondrial|P|Proteome|3348809	the glycine cleavage system catalyzes the degradation of glycine. the h protein shuttles the methylamine group of glycine from the p protein to the t protein.	mitochondrial .

||GGCX||GC|| gamma-glutamyl carboxylase|| EC 6.4.-.- ||VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE||	2677	NM_000821	NP_000812	Gamma-glutamyl carboxylase; vitamin K-dependent carboxylase	process|blood coagulation|E|GO:0007596|Proteome|9845520//cellular component|membrane fraction|P|GO:0005624|Proteome|1749935//biological process|protein modification|E|GO:0006464|Proteome|1749935//cellular component|integral membrane protein|P|GO:0016021|Proteome|1749935//molecular function|gamma-glutamyl carboxylase|E|GO:000848	organismal role|Blood clotting|E|Proteome|9845520//biochemical function|Transferase|E|Proteome|1749935//molecular localization|Integral membrane|P|Proteome|1749935//subcellular localization|Unspecified membrane|P|Proteome|1749935	vitamin k-dependent carboxylation of multiple amino-terminal glutamic acid residues in various proteins, it converts glutamate residues to gamma-carboxyglutamate.

||GGH||GH||EC 3.4.19.9||GAMMA-GLU-X CARBOXYPEPTIDASE|| GAMMA-GLUTAMYL HYDROLASE PRECURSOR||gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) precursor||	8836	NM_003878	NP_003869	Gamma-glutamyl hydrolase; has greater exopeptidase activity on methotrexate pentaglutamate than on diglutamate	molecular function|exopeptidase|E|GO:0008238|Proteome|8816764//molecular function|gamma-glutamyl hydrolase|E|GO:0008464|Proteome|8816764	biochemical function|Hydrolase|E|Proteome|8816764 //biochemical function|Protease (other than proteasomal)|E|Proteome|8816764	the polyglutamate sidechains of pteroylpolyglutamates. progressively removes gamma-glutamyl residues from pteroylpoly-gamma-glutamate to yield pteroyl-alpha-glutamate (folic acid) and free glutamate. may play an important role in the bioavailability of dietary pteroylpolyglutamates and in the metabolism of pteroylpolyglu	extracellular or lysosomal. while its intracellular location is primarily the lysosome, most of the enzyme activity is secreted.

||MEST||PEG 1||PATERNALLY EXPRESSED GENE 1||mesoderm specific transcript (mouse) homolog||MESODERM-SPECIFIC TRANSCRIPT, MOUSE, HOMOLOG OF||	4232	NM_002402	NP_002393	Mesoderm specific protein; member of the alpha/beta hydrolase fold family	biological process|mesoderm development|E|GO:0007498|Proteome|9158153	organismal role|Embryonic development|P|Proteome|9158153	
||PGK1P2||3-@PHOSPHOGLYCEROKINASE||PGK1||PGKA||PGK1P1||PRP2||EC 2.7.2.3||PRIMER RECOGNITION PROTEIN 2||PHOSPHOGLYCERATE KINASE 1 PSEUDOGENE 2||PGKA PHOSPHOGLYCERATE KINASE 1 PSEUDOGENE 1||	5230	NM_000291	NP_000282	Phosphoglycerate kinase 1; functions in glycolysis, converts 1,3-diphosphoglycerate to 3-phosphoglycerate	molecular function|phosphoglycerate kinase|E|GO:0004618|Proteome|7391028	biochemical function|Transferase|E|Proteome|6188151//biochemical function|Other kinase|E|Proteome|6188151	in addition to its role as a glycolytic enzyme, it seems that pgk-1 acts as a polymerase alpha cofactor protein (primer recognition protein).

molecular function|receptor|P|GO:0004872|Proteome|7503749//cellular component|membrane fraction|P|GO:0005624|Proteome|75037 49//cellular component|integral membrane protein|P|GO:0005887|Prot eome|750374 9	‖MMA‖MMD|macrophage maturation-associated‖MONOCYTE-TO-MACROPHAGE DIFFERENTIATION-ASSOCIATED PROTEIN‖monocyte to macrophage differentiation-associated, precursor‖	23531	NM_012329	NP_036461	Putative transmembrane protein	molecular localization|Integral membrane|Unspecified membrane|Proteome|7503749

biological process|visio n|E|GO:0007 601|Proteom e|10802664// molecular function|prote oglycan|P|G O:0005203|P roteome|755 8030//cellular componentle xtracellular matrix|E|GO: 0005578|Prot eome|766561 6//biological process|cartil age condensation |NR|GO:0001 502|Proteom e|na//molecul ar function|extra cellular matrix (cuticle and basement membrane)| NR|Proteome 207|Proteom e|na	organismal role|Extracell ular matrix component|N R|Proteome|7 665616//subc ellular localization|E xtracellular (excluding cell wall)|NR|Prot eome|766561 6//organismal role|Connecti ve Tissue Development and Maintenance| NR|Proteome |7665616//su bcellular localization|E xtracellular matrix (by similarity).	Lumican; extracellular matrix protein; member of the specialized collagens and SLRP_family	NP_002336	NM_002345	4060	||LUM||LDC||L UMICAN PRECURSO R||KERATAN SULFATE PROTEOGL YCAN||			

biological process|post-replication repair|P|GO:0006301|Proteome|1559696|molecular function|ubiquitin conjugating enzyme|P|GO:0004840|P	cellular role|DNA repair|NR|Proteome|15596 96|biochemical function|Protein conjugation factor|NR|Proteome|15596 96	catalyzes the covalent attachment of ubiquitin to other proteins. required for postreplication repair of uv-damaged dna.
||HHR6A||UBC2||HR6A||UBE2A||RAD6A||UBIQUITIN-PROTEIN LIGASE||EC 6.3.2.19||UBIQUITIN CARRIER PROTEIN||UBIQUITIN-CONJUGATING ENZYME E2-17 KDA||ubiquitin-conjugating enzyme E2A (RAD6 homolog)||RAD6, YEAST, HOMOLOG OF, TYPE A||	Human homolog of S. cerevisiae ubiquitin conjugating enzyme Rad6p; may catalyze ubiquitination of cellular proteins	7319 NM_003336 NP_003327

||NTS||NT/NMN||neurotensin precursor||NEUROTENSIN/NEUROMEDIN N PRECURSOR||	4922	NM_006183	NP_006174	Proneurotensin (proneuromedin N); precursor of the neuromodulating hormone neurotensin	cellular component|soluble fraction|P|GO:0005625|Proteome|8954810//molecular function|peptide hormone|NR|GO:0005180|Proteome|na//biological process|signal transduction|NR|GO:0007165|Proteome|na	molecular localization|Soluble|P|Proteome|8954810//organismal role|Neuronal transmission|NR|Proteome|8075503	neurotensin may play an endocrine or paracrine role in the regulation of fat metabolism. it causes contraction of smooth muscle.	secreted; packaged within secretory vesicles.

||MKI67||KIA||ANTIGEN KI-67||PROLIFERATION-RELATED Ki-67 ANTIGEN||antigen identified by monoclonal antibody Ki-67||	4288	NM_002417	NP_002408	Ki-67 antigen; may be required for proliferation; has numerous repeated elements	cellular component|nucleus|NR|GO:0005634|Proteome|na//cellular component|nucleolus|NR|GO:0005730|Proteome|na//biological process|cell cycle control|P|GO:0000074|Proteome|8227122//biological process|cell proliferation|E|GO:0008283|Proteome|8227122	localization|Nuclear|NR|Proteome|10878014//biochemical function|DNA-binding protein|P|Proteome|10878014//subcellular localization|Nuclear nucleolus|NR|Proteome|2571566//cellular role|Chromatin/chromosome structure|P|Proteome|10878014//organismal role|Control of Cell Proliferation|P|Proteome|10878014//molecular localization|D	thought to be required for maintaining cell proliferation.	nuclear. predominantly localized in the g1 phase in the perinucleolar region, in the later phases it is also detected throughout the nuclear interior, being predominantly localized in the nuclear matrix. in mitosis, it is present on all chromosomes.

||GPNMB||H									
GFIN||NMB||t									
ransmembra									
ne									
glycoprotein||		cellular							
GLYCOPRO		component|in							
TEIN		tegral							
NMB||glycopr		membrane							
otein		protein|P|GO:							
(transmembr		0016021|Prot							
ane)		eome|781415							
nmb||PUTATI		5//biological							
VE		process|nega							
TRANSMEM		tive control of	organismal						
BRANE	Similar to	cell	role|Control						
PROTEIN	melanocyte-	proliferation|	of Cell	could be a	type i			
NMB	specific	E|GO:000828	Proliferation|	melanogenic	membrane			
PRECURSO	protein	5|Proteome|7	P|Proteome|7	enzyme (by	protein				
R||	pMEL17	814155	814155	similarity).	(potential).				
	NP_002501								
	NM_002510								
	10457								

||HPRT||HPRT1||HGPRTASE||HGPRT||EC 2.4.2.8||HPRT1||HPRT||XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE||HYPOXANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE 1||hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)||	3251	NM_000194	NP_000185	Hypoxanthine phosphoribosyltransferase 1; involved in purine salvage pathway	function|hypoxanthine phosphoribosyltransferase|GO:0006166|Proteome|630	biological process|behavior|P|GO:0007610|Proteome|8485579||biological process|purine salvage|E|GO:0006166|P|Proteome|6300847	cytoplasmic.

||MMP1||CLG||CLGN||MMP-1||MATRIX METALLOPROTEINASE-1||fibroblast collagenase||EC 3.4.24.7||COLLAGENASE, INTERSTITIAL||COLLAGENASE, FIBROBLAST||INTERSTITIAL COLLAGENASE PRECURSOR||matrix metalloproteinase 1 preproprotein||matrix metalloproteinase 1 (interstitial collagenase)||	4312	NM_002421	NP_002412	Interstitial collagenase, a matrix metalloprotease; downregulated by transforming growth factor-beta 1 (TGFB1) or retinoic acid	molecular function|collagenase|E|GO:0008133|Proteome|3027129//molecular function|zinc binding|P|GO:0008270|Proteome|2167156//cellular component|extracellular space|NR|GO:0005615|Proteome|na//biological process|proteolysis and peptidolysis|P|GO:0006508|Proteome|2167156	cellular role|Protein degradation|NR|Proteome|2167156//organismal role|Extracellular matrix maintenance|NR|Proteome|2167156//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|2167156//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|3027129	cleaves collagens of types i, ii, and iii at one site in the helical domain. also cleaves collagens of types vii and x.

||CKS-2||CKS2||CDC2-ASSOCIATED PROTEIN CKS2||CDC28 protein kinase 2||CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2||CKS1(S. cerevisiae Cdc28/Cdc2 kinase subunit) homolog-2||	1164	NM_001827	NP_001818	Similar to S. pombe p13suc1; binds and regulates CDK-cyclin complexes	biological process|cell proliferation|PIGO:0008283|Proteome|8211159|biological	biological process|regulation of CDK activity|EIGO:0000079|Proteome|222741	biochemical function|Regulatory subunit|EIPro teome|82111 59	binds to the catalytic subunit of the cyclin dependent kinases and is essential for their biological function.	1
||TMEPAI||PMEPA1 protein||transmembrane, prostate androgen induced RNA||	56937	AF305616	NP_064567						

4||HSN3||HSBPROS26||EC 3.4.25.1||MACROPAIN BETA CHAIN||PROTEASOME CHAIN 3||PROTEASOME BETA CHAIN||PROTEASOME SUBUNIT, BETA-TYPE, 4||MULTICATALYTIC ENDOPEPTIDASE COMPLEX BETA CHAIN||Proteasome subunit, beta type, 4||PROTEASOME SUBUNIT BETA TYPE 4 PRECURSO	5692	NM_002796	NP_002787	Beta subunit 4 of the proteasome (prosome macropain)	cellular component|26S proteasome|P|GO:0005837|Proteome|8811196	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|7918633	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity.

||AIF4||ITCH|| NAPP1||AIP4 ||ATROPHIN-1- INTERACTING PROTEIN 4||NFE2-ASSOCIATED POLYPEPTIDE 1||atrophin-1 interacting protein 4||ITCHY, MOUSE, HOMOLOG OF||itchy (mouse homolog) E3 ubiquitin protein ligase||	83737 NM_031483 NP_113671	||CCNE1||CCNE||G1/S-SPECIFIC CYCLIN E1||	898 NM_001238 NP_476530	essential for the control of the cell cycle at the g1/s (start) transition. nuclear.

1||ANGIE||BC A1||SCYB13|| CXCL13||B-LYMPHOCY TE CHEMOATT RACTANT||B CELL-ATTRACTIN G CHEMOKINE 1||CXC CHEMOKINE LIGAND 13||SMALL INDUCIBLE CYTOKINE SUBFAMILY B, MEMBER 13||B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)||small inducible cytokine B subfamily (Cys-X-Cys	10563	NM_006419	NP_006410	4	4q21	Predicted B cell lymphocyte chemoattractant; chemotactic cytokine (chemokine)	function|chemokine|E|GO:0008009|Proteome|94866|51//biological process|chemotaxis|E|GO:0006935|Proteome|948|6651//biological process|immune response|E|GO:0006955|Proteome|948|6651//cellular component|soluble fraction|P|GO:0005625|Proteome|94866|51//biological process|cell-cell signalling|P|GO:0007267|Proteome|948|6651//biological process|inflammatory response|NR|Proteome|94866|51//biological process|cell-cell signalling|P|Proteome|9486651//organismal role|Cell-to-cell signalling|P|Proteome|948|6651	molecular localization|Soluble|P|Proteome|948665|1//organismal role|Anti-pathogen response|NR|Proteome|94866|51//biological process|cell-cell migration/motility|P|Proteome|9486651//organismal role|Cell-to-cell signalling|P|Proteome|948|6651

||C4BP||C4BPA||PRP||C4BPAL1||C4b RECEPTOR||PROLINE-RICH PROTEIN||C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR||Complement component 4-binding protein, alpha polypeptide||C4BP COMPLEMENT COMPONENT 4-BINDING PROTEIN, ALPHA-LIKE 1||	722	NM_000715	NP_000706	1 1q32	Complement component 4-binding protein, alpha; regulates the classical complement pathway; has regions common to Ba region in factor B and beta-2-glycoprotein and eight short consensus repeats	cellular component|extracellular space|NR|GO:0005615|Proteome|na	organismal role|Anti-pathogen response|NR|Proteome|3840370	the classical pathway of complement activation. it binds as a cofactor to c3b/c4b inactivator (c3bina), which then hydrolyzes the complement fragment c4b. it also accelerates the degradation of the c4bc2a complex (c3 convertase) by dissociating the complement fragment c2a. alpha chain binds c4b. it interacts also with

||IBP1||IGFB P1||IBP-1||PP12||IGF BP-1||IGF-BP25||PLAC ENTAL PROTEIN 12||IGF-BINDING PROTEIN 1||INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN 1||INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR||	3484	NM_000596	NP_000587	7	7p13-p12	Low molecular weight insulin-like growth factor binding protein 1; binds to and potentiates insulin-like growth factor activity; contains an RGD sequence	biological process|signal transduction|EC|GO:0007165|Proteome|2454104//cellular component|extracellular space|EC|GO:0005615|Proteome|245410 4//molecular function|insulin-like growth factor binding|EC|GO:0005520|Proteome|24541 04	organismal role|Control of Cell Proliferation|NR|Proteome|2461294//subcellular localization|extracellular (excluding cell wall)|NR|Proteome|245410 4	igf-binding proteins prolong the half-life of the igfs and have been shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptors.	secreted.

12 12q13.1

NP_076961
NM_024056
79022
||hypothetical protein MGC5576||

CYB11||B-R1||I-TAC||ITAC||IP-9||BETA-R1||CXCL11||SCYB9B, FORMERLY||INTERFERON-GAMMA-INDUCIBLE PROTEIN-9||INTERFERON-GAMMA-INDUCIBLE PROTEIN 9||CXC CHEMOKINE LIGAND 11||INTERFERON-INDUCIBLE T-CELL ALPHA CHEMOATTRACTANT||SMALL INDUCIBLE CYTOKINE B11 PRECURSOR||SMALL	6373	NM_005409	NP_005400	4 4q21.2	Cytokine B11; CXC chemokine that has chemotactic activity on activated T cells	function|chemokine|E|GO:0008009|Proteome|10233762//biological process|chemotaxis|E|GO:0006935|Proteome|10233762//biological process|signal transduction|P|GO:0007165|Proteome|10233762//biological process|cell-cell signalling|E|GO:0007267|Proteome|10233762//biological process|inflammatory response|P|GO:0006954|Proteome|102	organismal role|Response to injury|NR|Proteome|10233762//organismal role|Anti-pathogen response|NR|Proteome|10233762//organismal role|Cell migration/motility|NR|Proteome|10233762//organismal role|Cell-to-cell signalling|NR|Proteome|10233762	chemotactive for interleukin-activated t cells but not unstimulated t cells, neutrophils or monocytes. induces calcium release in activated t cells. binds to cxcr3. may play an important role in cns diseases which involve t cell recruitment. may play a role in skin immune responses.	secreted.

Highly similar to rat Castration Induced Prostatic Apoptosis Related protein-1	4 4q13.3-q21.3	protein-1	Related	Apoptosis	Prostatic	Induced	Castration	to rat	Highly similar		
		NP_056208									
		NM_015393									
		25849									
		‖DKFZP564 O0823 protein‖									
											AF098485
Region of low similarity to S. cerevisiae GRD19; may act as a signaling protein; contains a PX (Phox) domain	7 7p21.1										
Member of the phosphatidic acid (PA) phosphatase-related phosphoester ase family	9 9q31.1										
		NP_037454									
		NM_013322									
		29887									
‖SNX10‖sorti ng nexin 10‖											
		NP_060223									
		NM_017753									
		54886									
‖hypothetical protein FLJ20300‖											

||hepassocin||FGL1||HFREP1||HP-041||HFREP-1||fibrinogen-like 1 precursor||HEPATOCYTE-DERIVED FIBRINOGEN-RELATED PROTEIN 1||	2267	NM_004467	NP_004458	8	8p22-p21.3	Similar to the beta and gamma subunits of fibrinogen; lacks fibrinogen platelet-binding, x-linking, and thrombin-sensitive regions	cellular component|fibrinogen|PIGO:0005577|Proteome|839 0249//molecular function|fibrinogen|NR|GO:0008001|Proteome|na	has hepatocyte mitogenic activity.	secreted.

||INCAM-100||VCAM1||L1CAM||V-CAM 1||CD106 ANTIGEN||vascular cell adhesion molecule 1||VASCULAR CELL ADHESION PROTEIN 1 PRECURSOR||	7412	NM_001078	NP_542413	1	1p32-p31	Vascular cell adhesion molecule 1; functions as a cell surface adhesive molecule, binds specific blood leukocytes and tumor cells	molecular function|cell adhesion|NR|GO:0005194|Proteome|na/ /cellular component|plasma membrane|NR|GO:0005886|Proteome|na	organismal role|Blood clotting|NR|Proteome|1715583//biochemical function|Adhesin/agglutinin|NR|Proteome|1715583	important in cell-cell recognition. appears to function in leukocyte-endothelial cell adhesion. interacts with the beta-1 integrin vla4 on leukocytes, and mediates both adhesion and signal transduction. the vcam1/vla4 interaction may play a pathophysiologic role both in immune responses and in leukocyte emigration to sites of inflammation.	type i membrane protein.

||BMP-5||BMP5||BONE MORPHOGENETIC PROTEIN 5 PRECURSOR||	653	NM_021073	NP_066551	6	6p11.1	Bone morphogenetic protein 5; signals through receptor serine/threonine kinases; member of the TGF-beta family of growth factors	molecular localization|Soluble|NR|Proteome|na	induces cartilage and bone formation.
||XAGE-1 protein||	9503	NM_133431	XP_597674	X	Xp11.22-p11.21			

	140823	NM_080748	NP_542786	20	20q11.21			
‖FLJ22645‖ NMES1‖normal mucosa of esophagus specific 1‖	84419	NM_032413	NP_115789	15	15q14			
‖CRLF1‖CLF-1‖NR6‖CLF1 ‖cytokine receptor-like factor 1‖	9244	NM_004750	NP_004741	19	19p12	Similar to cytokine type 1 receptors	molecular function|receptor|P|GO:0004872|Proteome|9686600//cellular component|extracellular space|E|GO:0005615|Proteome|9686600//biological process|antimicrobial humoral response|P|GO:0006960|Proteome|9686600	organismal role|Anti-pathogen response|P|Proteome|9686600//biochemical function|Receptor (signalling)|NR|Proteome|9686600//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|9686600

OPGLG||RANKL||TRANCE||OPGL||TNFSF11||ODF||osteoprotegerin ligand||OSTEOCLAST DIFFERENTIATION FACTOR||TNF-related activation-induced cytokine||osteoclast differentionation factor||RECEPTOR ACTIVATOR OF NK-KAPPA-B LIGAND||TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11||tumor	8600	NM_003701	NP_143026	13	13q14	Type II membrane protein; binds receptor activator of NF-kappaB RANK (TNFRSF11A); contains a type II transmembrane domain	function|ligand|P|GO:0005102|Proteome|9367155//molecular function|cytokine|NR|GO:0005125|Proteome|na//biological process|immune response|P|GO:0006955|Proteome|9312132//biological process|signal transduction|P|GO:0007165|Proteome|9312132//biological process|skeletal development|E|GO:0001501|Proteome|9568710//cellular	organismal role|Anti-pathogen response|P|Proteome|9367155//molecular localization|Integral membrane|NR|Proteome|9312132//organismal role|Bone Development and Maintenance|E|Proteome|9568710	binds to tnfrsf11b/opg and to tnfrsf11a/rank. osteoclast differentiation and activation factor. augments the ability of dendritic cells to stimulate naive t-cell proliferation. may be an important regulator of interactions between t cells and dendritic cells and may play a role in the regulation of the t cell-dependent immune response. may also play an important	type ii membrane protein (isoforms 1 and 3); secreted (isoform 2). a soluble form of isoform 1 arises by proteolytic processing (by similarity).

||KIAA0145||DGKD||DAGK4-PEN||DGKdelta||DGK-DELTA||DIGLYCERIDE KINASE||EC 2.7.1.107||DAG KINASE DELTA||DGK ISOZYME, 130-KD||DIACYLGLYCEROL KINASE, DELTA, 130-KD||diacylglycerol kinase, delta (130kD)||130 KDA DIACYLGLYCEROL KINASE||	8527	NM_003648	NP_003639	2 2q37.1	Diacylglycerol kinase delta; phosphorylates the arachidonoyl type of diacylglycerol; contains a pleckstrin homology domain and an EPH domain	biological process|sign al transduction|E|GO:000716 5|Proteome|8626538//molecular function|diacylglycerol kinase|E|GO:0004143|Proteome|862653 8	biochemical function|Transferase|E|Proteome|86265 38//biochemical function|Other function|cytoplasmic. can be loosely bound to the membranes.

				7				
||hypothetical protein MGC10981||	84740	NM_032654	NP_116043	4 4p16.1				BC028141
||GTPBP2||GTP binding protein 2||	54676	NM_019096	NP_061969	6 6p21-p12	Putative GTP binding protein 2; member of the GP-1 family of GTPases	molecular function|GTPase|P|GO:0003924|Proteome|10833435//biological process|small GTPase mediated signal transduction|P|GO:0007264|Proteome|10833435	biochemical function|Hydrolase|P|Proteome|10833435//biochemical function|GTP-binding protein/GTPase|P|Proteome|10833435	BC014103

||GalNAcT2|| GALNT2||2.4.1.41||UDP-GalNAc transferase 2||UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)||	2590	NM_004481	NP_004472		1	1q41-q42	biological process|O-UDP-N-acetyl-linked alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2; catalyzes O-glycosylation of serine and threonine residues	biochemical function|Transferase|EC:0.0.0.0|Proteome|9592121 21		

||CRL1||WSX 1||TCCR||WSX-1||T-cell cytokine receptor||class I cytokine receptor||	9466	NM_004843	NP_004834	19	19p13.11	Member of the class I cytokine receptor family; may be involved in the modulation of the immune response	biological process|immune response|P|GO:0006955|Proteome|9600072//molecular function|transmembrane receptor|P|GO:0004888|Proteome|9600072//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9600072//biological process|cell surface receptor linked signal transduction|P|GO:0007166|Proteome|9600072	organismal role|Anti-pathogen response|P|Proteome|9600072//molecular localization|Integral membrane|P|Proteome|9600072//biochemical function|Receptor (signalling)|P|Proteome|9600072

||hypothetical protein FLJ22530||	BC001171	79619	1 1q12	||FADS1||FADS2||D5D||TU12||LLCDL1||delta-5 desaturase||delta-5 fatty acid desaturase|||linoleoyl-CoA desaturase (delta-6-desaturase)-like 1||fatty acid desaturase 1||	3992	NM_013402	NP_037534	11q12.2-11 q13.1	Delta-5 desaturase; catalyzes production of polyenic fatty acids such as arachidonic acid	molecular function|C-5 sterol desaturase|EC:0000248|Proteome|10601301//biological process|fatty acid desaturation|EC:000663 6|Proteome|1 0601301//cellular component|integral membrane protein|P|GO:0016021|Prot eome|106013 01	biological process|digestion|P|GO:0007586|Proteome|2674141 //biological process|proteolysis and peptidolysis|NR|GO:0006508|Proteom e|na	Cathepsin E; gastric aspartyl protease (acid protease)	1510	NM_001910	NP_001901	1 1q31	||CTSE||EC 3.4.23.34||CATHEPSIN E PRECURSOR||	due ot its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function.

||IFI17||IFITM 1||9-27||LEU13||LEU-13 ANTIGEN||interferon-induced protein 17||INTERFERON-INDUCIBLE PROTEIN 9-27||INTERFERON-INDUCED TRANSMEMBRANE PROTEIN 1||interferon induced transmembrane protein 1 (9-27)||	8519	NM_003641	NP_003632	11	11	Interferon-inducible transmembrane protein 1; involved in relaying antiproliferative and homotypic adhesion signals	component|plasma membrane|E|GO:0005886|Proteome|7559564//biological process|cell cycle control|P|GO:0000074|Proteome|7559564//molecular function|receptor signalling protein|P|GO:0005057|Proteome|7559564//biological process|negative control of cell proliferation|P|GO:0008285|Proteome|7559564//biological process|cell surface receptor	biochemical function|Receptor (signalling)|NR|Proteome|7559564//organismal role|Control of Cell Proliferation|NR|Proteome|7559564	implicated in the control of cell growth. component of a multimeric complex involved in the transduction of antiproliferative and homotypic adhesion signals.	integral membrane protein (potential).

||PCDH3X||PCDH-BETA-16||protocadherin-3x||KIAA1621||PCDH-BETA16||PCDHB16||ME1|PROTOCADHERIN-BETA 16||cadherin ME1|||protocadherin beta 8a||protocadherin beta 16 precursor||	57717	NM_020957	NP_066008	5 5q31

ARCA1||SNF2LB||SWI2||SNF2-LIKE 1||POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1||SUCROSE NONFERMENTING, YEAST, HOMOLOG-LIKE 1||SNF2 (sucrose nonfermenting, yeast, homolog)-like 1||SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY	6594	NM_003069	NP_620604	X	Xq25	Member of SWI/SNF related family of proteins; may regulate transcription via its effects on chromatin structure	cellular component|nucleus|P|GO:0005634|Proteome|1408766//molecular function|helicase|P|GO:0004386|Proteome|1408766//biological process|chromatin modelling|P|GO:0006338|Proteome|1408766//molecular function|adenosinetriphosphatase|P|GO:0004002|Proteome|1408766	biochemical function|Hydrolase|P|Proteome|1408766//subcellular localization|Nuclear|P|Proteome|1408766//cellular role|Chromatin/chromosome structure|P|Proteome|1408766//molecular localization|DNA-associated (direct or indirect)|P|Proteome|1408766		nuclear.

ARCA1||SNF2LB||SWI2||SNF2-LIKE 1||POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1||SUCROSE NONFERMENTING, YEAST, HOMOLOG-LIKE 1||SNF2 (sucrose nonfermenting, yeast, homolog)-like 1||SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY	6594	NM_003069	X NP_620604	Xq25	Member of SWI/SNF related family of proteins; may regulate transcription via its effects on chromatin structure	Proteome|1408766||Molecular function|helicase|P|GO:0004386|Proteome|1408766||Cellular biological process|chromatin modelling|P|GO:0006338|Proteome|1408766	biochemical function|Hydrolase|P|GO:0004002|Proteome|1408766	cellular component|nucleus|P|GO:0005634|Proteome|1408766||Molecular function|helicase|P|GO:0004386|Proteome|1408766||Cellular biological process|chromatin modelling|P|GO:0006338|Proteome|1408766	role|Chromatin remodeling|P|GO: (direct or indirect)|P|Proteome|1408766	nuclear.

||LBR||LMN2R||lamin B receptor||INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN||	3930	NM_002296	NP_002287	1	1q42.1	Lamin B receptor; may mediate interaction between chromatin and lamin B; contains eight putative transmembrane domains	molecular function|DNA binding|E|GO:0003677|Proteome|8157662//molecular function|lamin binding|E|GO:0005521|Proteome|8157662//molecular function|lamin/chromatin binding|E|GO:0003683|Proteome|8157662//cellular component|nuclear inner membrane, integral protein|E|GO:0005639|Proteome|8157662	localization|Nuclear matrix|E|Proteome|8157663//biochemical function|DNA-binding protein|E|Proteome|8157662//molecular localization|Integral membrane|E|Proteome|8157663//cellular role|Chromatin/chromosome structure|P|Proteome|8157662//molecular localization|DNA-associated (direct or indirect)|E|Proteome|8157662	anchors the lamina and the heterochromatin to the inner nuclear membrane. can interact with chromodomain proteins.	nuclear envelope inner membrane.

||CDC25HU2||EC 3.1.3.48||M-PHASE INDUCER PHOSPHATASE 2||DUAL SPECIFICITY PHOSPHATASE CDC25B||cell division cycle 25B, isoform 4||cell division cycle 25B, isoform 1||cell division cycle 25B, isoform 2||cell division cycle 25B, isoform 3||	994	NM_021874	NP_068660	20 20p13	Tyrosine phosphatase; triggers activation of CDC2 by removing inhibitory phosphate	biological process|mitosis|E|GO:0007067|Proteome|1836978//biological process|cell cycle control|P|GO:0000074|Proteome|1836978//molecular function|protein tyrosine phosphatase|E|GO:0004725|Proteome|1836978//biological process|positive control of cell proliferation|P|GO:0008284|Proteome|8276402	biochemical function|Hydrolase|E|Proteome|1836978//organismal role|Control of Cell Proliferation|P|Proteome|8276402	functions as a dosage-dependent inducer in mitotic control. it is a tyrosine protein phosphatase required for progression of the cell cycle. it directly dephosphorylates cdc2 and activate its kinase activity. the three isoforms seem to have a different level of activity.

||MTRR||2.1.1.135||MSR||5-methyltetrahydrofolate-homocysteine methyltransferase reductase||methionine synthase reductase, isoform 1||methionine synthase reductase, isoform 2||methionine synthase]-cobalamin methyltransferase (cob(II)alamin reducing)||	4552	NM_024010	NP_076915	5	5p15.3-p15.2	Methionine synthase reductase; regenerates cobalamin cofactor needed for active methionine synthase	molecular function|electron transporter|P|GO:0005489|Proteome|95 01215|biological process|amino acid metabolism|P|GO:0006520|Proteome|95 01215	biochemical function|Oxidoreductase|E|Proteome|95 01215|cellular role|Amino-acid metabolism|E|Proteome|95 01215		

||Tyro11||MYK1||HTK||EphB4||EC 2.7.1.112||TYROSINE-PROTEIN KINASE RECEPTOR HTK||MYK, MOUSE, HOMOLOG OF||EPHRIN TYPE-B RECEPTOR 4 PRECURSOR||Ephrin receptor EphB4 (hepatoma transmembrane kinase)||	2050	NM_004444	NP_004435	7	7q22	Eph-related receptor tyrosine kinase B4; has extracellular fibronectin type-III domains, similar to murine Ephb4	biological process|cell proliferation|P|GO:0008283|Proteome|8152808//biological process|histogenesis and organogenesis|P|GO:0007397|Proteome|8831703//cellular component|integral plasma membrane protein|E|GO:0005887|Proteome|8188704//molecular function|transmembrane receptor protein tyrosine kinase|E|GO:0004714|Proteome|8188704	biochemical function|Transferase|E|Proteome|8188704//molecular localization|Integral membrane|E|Proteome|8188704//biochemical function|Receptor (signalling)|E|Proteome|8188704	receptor for members of the ephrin-b family. binds to ephrin-b2. may have a role in events mediating differentiation and development.	type i membrane protein.

||LAK-4P||expressed in activated T/LAK lymphocytes||	11322	AK074065	NP_009198	17 17q25
||hypothetical protein MGC2840 similar to a putative glucosyltransferase||	79053	NM_024079	NP_076984	11 11pter-p15.5
||PDCR||DECR2||peroxisomal 2,4-dienoyl-CoA reductase||2,4-dienoyl CoA reductase 2, peroxisomal||	26063	NM_020664	NP_065715	16 16p13.12

LERK1||ECK LG||EFNA1|| TNFAIP4||EP GL1||LERK-1||EPLG1||EP HRIN-A1 PRECURSO R||ephrin A1 precursor||LI GAND OF EPH-RELATED KINASE 1||TUMOR NECROSIS FACTOR-ALPHA-INDUCED PROTEIN 4||IMMEDIAT E EARLY RESPONSE PROTEIN B61||eph-related receptor tyrosine kinase ligand 1 (tumor necrosis factor, alpha-	1942	NM_004428	NP_004419	molecular function|ligand|P|GO:0005102|Proteome|233719|biological process|cell-cell signalling|P|GO:0007267|Proteome|866 0976|molecular function|transmembrane-ephrin|P|GO:0005108|Prot eome|866097 6|cellular componentlin	1	1q21-q22	Ephrin-A1; ligand of Eph-related receptor tyrosine kinases	organismal role|Cell-to-cell signalling|NR|Proteome|86 60976|molecular tegral plasma membrane protein|P|GO: tegral 0005887|Prot eome|866097 6	localization|In attached to the membrane by a gpi-anchor. membrane|N R|Proteome|8 660976

AC-1||MIP4||MIP-4||PARC||SCYA18||DC-CK1||DCCK1||chemokine (C-C), dendritic||CC CHEMOKINE PARC||PULMONARY AND ACTIVATION-REGULATED CHEMOKINE||MACROPHAGE INFLAMMATORY PROTEIN 4||DENDRITIC CELL CHEMOKINE 1||SMALL INDUCIBLE CYTOKINE A18 PRECURSOR||ALTERNATIVE MACROPHA	6362	NM_002988	NP_002979	17	17q11.2	Cytokine A18; chemokine that has a prederential activity for na□ve T lymphocytes	function|chemokine|E|GO:0008009|Proteome|9192897//biological process|chemotaxis|E|GO:0006935|Proteome|9192897//biological process|immune response|P|GO:0006955|Proteome|9192897//biological process|cell communication|P|GO:0007154|Proteome|9192897//biological process|signal transduction|E|GO:0007165|Proteome|9233607//biological	molecular localization|Soluble|NR|Proteome|9233607//organismal role|Anti-pathogen response|P|Proteome|9233607//organismal role|Cell migration/motility|NR|Proteome|9233607//organismal role|Cell-to-cell signalling|NR|Proteome|9233607	factor that attracts lymphocytes but not monocytes or granulocytes. may be involved in b cell migration into b cell follicles in lymph nodes. attracts naive t lymphocytes toward dendritic cells and activated macrophages in lymph nodes, has chemotactic activity for naive t cells, cd4+ and cd8+ t cells and thus may play a role in both humoral and cell-mediated immunity	secreted.

1||CD54||CA								role|Protein
M1||MAJOR				molecular				translocation|
GROUP				function|rece				E|Proteome|2
RHINOVIRU				ptor|E|GO:00				538243//orga
S				04872|Proteo				nismal
RECEPTOR||				me|2538243//				role|Pathoge
INTERCELL				molecular				nic
ULAR				function|cell				Invasion|NR|
ADHESION				adhesion|NR|				Proteome|33
MOLECULE-				GO:0005194|				49522//bioch
1				Proteome|na/				emical
PRECURSO				/cellular				function|Adhe
R||cell				componentlpl				sin/agglutinin|
surface				asma				E|Proteome|3
glycoprotein				membrane|N				349522//orga
P3.58||interce				R|GO:00058				nismal
llular				86|Proteome|			role|Anti-
adhesion				na//molecular				pathogen
molecule 1			Surface	function|trans				response|NR|
precursor||AN			glycoprotein;	membrane				Proteome|10
TIGEN			binds the	receptor|E|G				985244//mole
IDENTIFIED			integrin LFA-	O:0004888|P				cular
BY			1 (ITGB2)	roteome|253				localization|In
MONOCLON			and	8243//cellular				tegral
AL			promotes	componentlin				membrane|P|
ANTIBODY			adhesion;	tegral plasma				Proteome|33
BB2||SURFA			member of	membrane				49522//bioch
CE			the	proteoglycan|			emical
ANTIGEN			immunoglobu	E|GO:000588				function|Rece
OF		19p13.3-	lin	8|Proteome|2				ptor (protein
ACTIVATED	3383	19 p13.2	superfamily	538243	NM_000201	NP_000192		translocation)

(integrin alpha-l/beta-2).

type i membrane protein.

AD-BETALIPOPROTEINEMIA||APO-E||FLOATING-BETALIPOPROTEINEMIA||HYPERLIPOPROTEINEMIA, TYPE III||APOLIPOPROTEIN E PRECURSOR||FAMILIAL HYPERCHOLESTEROLEMIA WITH HYPERLIPEMIA||FAMILIAL HYPERBETA-AND PREBETALIPOPROTEINEMIA||HYPERLIPEMIA WITH FAMILIAL HYPERCHOLESTEROLE	348	NM_000041	NP_000032	19	19q13.2	Apolipoprotein E; component of lipoproteins, ligand for low density lipoprotein receptor	function|ligand|P|GO:0005102|Proteome|9218423//biological process|circulation|P|GO:0008015|Proteome|9218423//molecular function|plasma protein|NR|GO:0005209|Proteome|na//biological process|immune response|NR|GO:0006955|Proteome|na//biological process|lipid metabolism|NR|GO:0006629|Proteome|na//molecular function|lipid transporter|NR|GO:0005319|Proteome|	cellular role|Differentiation|NR|Proteome|3283935//molecular localization|Soluble|NR|Proteome|3283935//organismal role|Neuronal development|NR|Proteome|3283935//organismal role|Anti-pathogen response|NR|Proteome|3283935//organismal role|Intercellular transport|NR|Proteome|na	apo-e mediates binding, internalization, and catabolism of lipoprotein particles. it can serve as a ligand for the ldl(apo b/e) receptor and for the specific apo-e receptor (chylomicron remnant) of hepatic tissues.	extracellular.

||PON2||EC 3.1.1.2||EC 3.1.8.1||paraoxonase 2||A-ESTERASE 2||PON 2||SERUM ARYLDIALKYLPHOSPHATASE 2||SERUM PARAOXONASE/ARYLESTERASE 2||AROMATIC ESTERASE 2||	5445	NM_000305	NP_000296	7 7q21.3	Paraoxonase /arylesterase 2; possibly functions in protecting low density lipoprotein against oxidative modification; member of a family that hydrolyzes toxic organophosphates	molecular function|arylesterase|P|GO:0004064|Proteome|8661009	biochemical function|Hydrolase|P|Proteome|8661009//cellular role|Other metabolism|P|Proteome|8661009	hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. capable of hydrolyzing a broad spectrum of organophosphate substrates and a number of aromatic carboxylic acid esters (by similarity).	extracellular (by similarity).

||HS2ST1||Kl AA0448||hep aran sulfate 2-O-sulfotransfera se 1||	9653	NM_012262	NP_036394	1	1p31.1-p22.1

||LACI||EPI||TFPI||TFPI1||EXTRINSIC PATHWAY INHIBITOR|| TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR||tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)||	7035	NM_006287	NP_006278	2	2q31-q32.1	Lipoprotein-associated coagulation inhibitor; a Kunitz-type protease inhibitor that inhibits fibrin clot formation	molecular function|plasma protein|NR|GO:0005209|Proteome|na//biological process|blood coagulation|E|GO:0007596|Proteome|9252393//molecular function|plasma glycoprotein|NR|GO:0005211|Proteome|na//molecular function|proteinase inhibitor|E|GO:0004866|Proteome|9252393	organismal role|Blood clotting|E|Proteome|9252393//biochemical function|Inhibitor or repressor|NR|Proteome|1993173//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|1993173	inhibits factor x (x(a)) directly and, in a xa-dependent way, inhibits vii(a)/tissue factor activity, presumably by forming a quaternary x(a)/laci/vii(a)/tf complex. it possesses an antithrombotic action and also the ability to associate with lipoproteins in plasma.	secreted.

||ADCY7||KIAA0037||EC 4.6.1.1||ATP PYROPHOSPHATE-LYASE||ADENYLYL CYCLASE||adenylate cyclase 7||ADENYLATE CYCLASE, TYPE VII||	113	NM_001114	NP_001105	16	16q12-q13	Adenylate cyclase (type 7), an ATP-pyrophosphate lyase; converts ATP to cAMP	cellular component|plasma membrane|P|GO:0005886|Proteome|7860067//biological process|signal transduction|P|GO:0007165|Proteome|7860067//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|7860067	molecular localization|integral membrane|P|Proteome|7860067	this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase.	integral membrane protein.
||ALEX3||ALEX3 protein||ARM PROTEIN LOST IN EPITHELIAL CANCERS, X CHROMOSOME, 3||	51566	NM_016607	NP_057691	X	Xq21.33-q22.2	Weakly similar to a region of yeast vacuolar protein Vac8p				

||AUP1||ANCI ENT UBIQUITOU S PROTEIN 1 PRECURSO R||	550	NM_012103	NP_036235	2 2p13	ubiquitously expressed protein	unknown|PIG O:0005554|P roteome|881 2468	molecular function|mole cular_functio n

3||DUSP6||PYST1||MKP3||EC 3.1.3.16||EC 3.1.3.48||DUAL-SPECIFICITY PHOSPHATASE 6||MAP kinase phosphatase 3||serine/threonine specific protein phosphatase||DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1||DUAL SPECIFICITY PROTEIN PHOSPHATASE 6||MITOGEN-ACTIVATED PROTEIN KINASE	1848	NM_001946	NP_073143	12	12q22-q23	Dual specificity protein phosphatase 6; selectively dephosphorylates and inactivates MAP kinase	component|cytoplasm|E|GO:0005737|Proteome|8670865//biological process|apoptosis|NR|GO:0006915|Proteome|na//biological process|MAPKKK cascade|NR|GO:0000165|Proteome|na//cellular component|soluble fraction|E|GO:0005625|Proteome|8670865//biological process|cell cycle control|NR|GO:0000074|Proteome|na//molecular function|protein	cellular role|Differentiation|P|Proteome|9205128//biochemical function|Hydrolase|E|Proteome|8670865//molecular localization|Soluble|E|Proteome|8670865//organismal role|Cell death/Apoptosis|P|Proteome|9205128//subcellular localization|Cytoplasmic|E|Proteome|8670865	inactivates map kinases. has a specificity for the erk family.	cytoplasmic.

||PRSC1||EC 3.4.22.34||LEGUMAIN PRECURSOR||ASPARAGINYL ENDOPEPTIDASE||protease, cysteine, 1 (legumain)||	5641	NM_005606	NP_005597	14	14q32.1	Legumain; cysteine endoprotease that hydrolyzes asparaginyl bonds	molecular function|legumain|P|GO:0001509|Proteome|9065484	biochemical function|Hydrolase|NR|Proteome|9065484//biochemical function|Protease (other than proteasomal)|NR|Proteome|9065484

C 3.1.1.34||LPL DEFICIENCY ||LIPD DEFICIENCY ||HYPERCHYLOMICRONEMIA, FAMILIAL||LIPASE D DEFICIENCY ||LIPOPROTEIN LIPASE DEFICIENCY ||HYPERLIPOPROTEINEMIA, TYPE IA||HYPERLIPEMIA, ESSENTIAL FAMILIAL||lipoprotein lipase precursor||HYPERLIPEMIA , IDIOPATHIC, BURGER-GRUTZ TYPE||CHYLOMICRONE	4023	NM_000237	NP_000228	8 8p22	Lipoprotein lipase; hydrolyses the triacylglycerol component of lipoproteins	biological process|circulation|E|GO:0008015|Proteome|1969408 //cellular component|extracellular|E|GO:0005576|Proteome|1969408//molecular function|heparin binding|E|GO:0008201|Proteome|1969408//molecular function|lipoprotein lipase|E|GO:0004465|Proteome|1969408//biological process|fatty acid metabolism|NR|GO:0006631|Proteome|na	biochemical function|Hydrolase|E|Proteome|7818530 //organismal role|Energy Storage|NR|Proteome|na	the primary function of this lipase is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (vldl). the enzyme functions in the presence of apolipoprotein c-2 on the luminal surface of vascular endothelium.	attached to the membrane by a gpi-anchor.

|SPINK1||PSTI||TUMOR-ASSOCIATED TRYPSIN INHIBITOR|| SERINE PROTEASE INHIBITOR, KAZAL-TYPE, 1||SERINE PROTEASE INHIBITOR KAZAL-TYPE 1||PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR||serine protease inhibitor, Kazal type 1||Serine protease inhibitor, Kazal type I (pancreatic secretory trypsin	6690	NM_003122	NP_003113	5 5q32	Kazal-type serine protease inhibitor; inhibits secreted pancreatic trypsin	molecular function|protease inhibitor|E|GO:0004866|Proteome|714 2173	biochemical function|inhibitor or repressor|NR|Proteome|35 01289	this is a trypsin inhibitor, its physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas.	secreted.

||CALDAG-GEFII||RASGRP1||RAS guanyl nucleotide-releasing protein 1||guanine nucleotide exchange factor, calcium- and DAG-regulated, Rap1A||RAS guanyl releasing protein 1 (calcium and DAG-regulated)||	10125	NM_005739	NP_005730	15 15q15	RAS guanyl releasing protein 1 (calcium and DAG-regulated); activates ras signaling; has Ca2+ and DAG binding domains	function|lipid binding|P|GO:0008289|Proteome|9582122//molecular function|calcium binding|P|GO:0005509|Proteome|9582122//cellular component|membrane fraction|E|GO:0005624|Proteome|9582122//biological process|signal transduction|E|GO:0007165|Proteome|9789079//biological process|RAS protein signal transduction|E|GO:0007265|Proteome|9582122//molecular

||GNA12||G ALPHA 12||GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-12 SUBUNIT||guanine nucleotide binding protein (G protein) alpha 12||	2768	AK025582	NP_031379	7	7p22-p21	G-protein alpha subunit 12; couples to thrombin and thromboxane A2 receptors in platelets	process|blood coagulation|P|GO:0007596|Proteome|8290554//molecular function|signal transduction|NR|GO:0004871|Proteome|na//biological process|cell growth and maintenance|E|GO:0008151|Proteome|8423800//molecular function|heterotrimeric G-protein GTPase, alpha subunit|E|GO:0000263|Proteome|8290554//biological process|G-	cellular role|Differentiation|E|Proteome|8423800//biochemical function|Hydrolase|E|Proteome|8290554//organismal role|Blood clotting|P|Proteome|8290554//biochemical function|GTP-binding protein/GTPase|E|Proteome|8290554	guanine nucleotide-binding proteins (g proteins) are involved as modulators or transducers in various transmembrane signaling systems.	membrane-bound.

component|cytoplasm|EIGO:0005737|Proteome|7796809//molecular function|cell adhesion|PIGO:0005194|Proteome|7796809//cellular component|fo cal adhesion|EIGO:0008357|Proteome|7796809//biologi cal process|sign al transduction|	Member of the alpha liprin family; may regulate disassembly of the adhesions, localizes PTPRF to focal adhesions	11	11q13.3		NP_003617	NM_003626	8500	||PPFIA1||LIP.1||protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1||

||TIF1ALPHA||TIF1||HTIF1||PTC6||TRIM24||TIF1A||TF1A||TIF1A PTC6 CHIMERIC ONCOGENE||TRANSCRIPTIONAL INTERMEDIARY FACTOR 1-ALPHA||transcriptional intermediary factor 1 alpha||	8805	NM_003852	NP_003843	7 7q32-q34	Mediates the activation function (AF-2) of nuclear estrogen receptor; also mediates activation function (AF-2) of other nuclear receptors	function|ligand|E|GO:0005102|Proteome|9115274//cellular component|nucleus|E|GO:0005634|Proteome|9115274//molecular function|transcription co-activator|E|GO:0003713|Proteome|9115274//molecular function|transcription activating factor|E|GO:0003710|Proteome|9115274//biological process|transcription from Pol II promoter|E|GO:0006366|Proteome|9115274//molecu	biochemical function|Activator|NR|Proteome|9115274//subcellular localization|Nuclear|NR|Proteome|9115274//cellular role|Pol II transcription|NR|Proteome|9115274//cellular role|Chromatin/chromosome structure|NR|Proteome|9191165//molecular localization|DNA-associated (direct or indirect)|NR|Proteome|9115274

||PPASE||OPPP|SID6-8061||PP||PYROPHOSPHATASE, INORGANIC|EC 3.6.1.1||inorganic pyrophosphatase||PYROPHOSPHATE PHOSPHO-HYDROLASE||pyrophosphatase (inorganic)||	5464	NM_021129	NP_066952	10 10q11.1-q24	Inorganic pyrophosphatase; catalyzes the hydrolysis of pyrophosphate to inorganic phosphate	biological process|phosphate metabolism|GO:0006796|Proteome|10542310	biochemical function|Hydrolase|P|Proteome|10542310//biochemical function|Other|Other|Proteome|10542310//biochemical function|Other|Proteome|10542310	cytoplasmic (by similarity).
||hypothetical protein FLJ11259||	55332	NM_018370	NP_060840	12 12q23.1				

C||PCK1||EC 4.1.1.32||PHOSPHOENOLPYRUVATE CARBOXYLASE||PEPCK DEFICIENCY, CYTOSOLIC||phosphoenolpyruvate carboxykinase 1 (soluble)||PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC [GTP]||PHOSPHOENOLPYRUVATE CARBOXYKINASE 1, SOLUBLE||PEPCK1 PHOSPHOENOLPYRUVATE CARBOXYKINASE	5105	NM_002591	NP_002582	20	20q13.31	Cytosolic phosphoenolpyruvate carboxykinase (GTP) 1; forms phosphoenolpyruvate by decarboxylation of oxaloacetate	cellular component|cytosol|NR|GO:0005829|Proteome|na//biological process|glucose metabolism|NR|GO:0006006|Proteome|na//molecular function|phosphoenolpyruvate carboxylase (GTP)|P|GO:0004613|Proteome|8490617	biochemical function|Lyase|E|Proteome|8490617//subcellular localization|Cytoplasmic|E|Proteome|1657985	cytoplasmic.

||LR8||LR8 protein||	28959	NM_014020	NP_054739	7	7q35	Expressed by a lung fibroblast subpopulation	biological process|histogenesis and organogenesis|P|GO:0007397|Proteome|9922225	
||RAIG1||RAI3||GPRC5A||RETINOIC ACID-INDUCED 3||retinoic acid induced 3||RETINOIC ACID-INDUCIBLE GENE 1||retinoic acid responsive gene||	9052	NM_003979	NP_003970	12	12p13-p12.3	Putative G protein-coupled receptor	biological process|signal transduction|P|GO:0007165|Proteome|9857033//molecular function|G-protein linked receptor|P|GO:0004930|Proteome|9857033//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9857033	molecular localization|Integral membrane|P|Proteome|9857033//biochemical function|Receptor (signalling)|P|Proteome|9857033

||SBBI42 protein||BCM-like membrane protein precursor||	56833	NM_020125	NP_064510	1	1q22			
||C2GNT-M||C2/4GNT||GnT-M||GCNT3||glucosaminyl (N-acetyl) transferase 3, mucin type||	9245	NM_004751	NP_004742	15	15q21.3	Mucin type beta-1,6-N-acetylglucosaminyltransferase (UDP-GlcNAc:Gal/GlcNAcbeta1-3GalNAcalpha beta1, 6GlcNAc-transferase); forms core 2, core 4 and I type O-glycan branches	cellular component|membrane fraction|P|GO:0005624|Proteome|9988682//biological process|O-linked glycosylation|E|GO:0006493|Proteome|9988682//biological process|carbohydrate metabolism|NR|GO:0005975|Proteome|na//molecular function|N-acetyllactosaminide beta-1,6-N-acetylglucosaminyltransferase|E|GO:0008109|Proteome|9988682	biochemical function|Transferase|E|Proteome|9988682//subcellular localization|Unspecified membrane|P|Proteome|9988682

||TIMM17A-PENDING||TIM17||TIM17A||preprotein translocase||translocase of inner mitochondrial membrane 17 (yeast) homolog A||TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 17, YEAST, HOMOLOG OF, A||	10440	NM_006335	NP_006326	1	1q32.1	Mitochondrial inner membrane translocase subunit; translocates nuclear-encoded proteins into the mitochondrion	cellular component|integral membrane protein|E|GO:0016021|Proteome|10339406//biological process|mitochondrial translocation|P|GO:0006628|Proteome|10339406//cellular component|integral plasma membrane protein|NR|GO:0005887|Proteome|na//cellular component|mitochondrial inner membrane translocase complex|E|GO:0005744|Proteome|10339406	cellular role|Protein translocation|P|Proteome|10339406//molecular localization|Integral membrane|NR|Proteome|10339406//biochemical function|Receptor (protein translocation)|P|Proteome|10339406

RTYLGLUCOSAMINURIA||AGU||GLYCOASPARAGINASE||ASPARTYLGLYCOSAMINURIA ASPARTYLGLUCOSAMINIDASE||EC 3.5.1.26||AGA DEFICIENCY||N4-(N-ACETYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE||GLYCOSYLASPARAGINASE DEFICIENCY||aspartylglucosaminidase precursor||ASPARTYLGLUCOSAMINID	175	NM_000027	NP_000018	4	4q32-q33	Lysosomal glycosylasparaginase (aspartylglucosaminidase N4-(beta-N-acetylglucosaminyl)-L-asparaginase); cleaves GlcNAc-Asn bonds in N-linked glycoproteins	cellular component|lysosome|NR|GO:0005764|Proteome|na//biological process|protein deglycosylation|P|GO:0006517|Proteome|2775174//molecular function|N4-(beta-N-acetylglucosaminyl)-L-asparaginase|E|GO:0003948|Proteome|1703489	biochemical function|Hydrolase|E|Proteome|2775174//cellular role|Protein degradation|E|Proteome|2775174//subcellular localization|Lysosome/vacuole|E|Proteome|1904874	cleaves the glcnac-asn bond which joins oligosaccharides to the peptide of asparagine-linked glycoproteins.	lysosomal.

||MICB||MHC class I polypeptide-related sequence B||MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I CHAIN-RELATED GENE B||	4277	NM_005931	NP_005922	6 6p21.3	Member of the MIC (MHC class I chain-related) family; may bind gamma delta T cells	biological process|stress response|E|GO:0006950|Proteome|9497295//molecular function|protein binding|P|GO:0005515|Proteome|8022771//biological process|cell recognition|E|GO:0008037|Proteome|9497295//biological process|cellular defense response|P|GO:0006968|Proteome|9497295	cellular role|Cell stress|P|Proteome|9497295//organismal role|Anti-pathogen response|NR|Proteome|9497295

||CPLA2-ALPHA||LYSOPHOSPHOLIPASE||CPLA2||PLA2G4A||EC 3.1.1.5||PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE||EC 3.1.1.4||CYTOSOLIC PHOSPHOLIPASE A2||PHOSPHOLIPASE A2, CYTOSOLIC, CALCIUM-DEPENDENT, ALPHA||phospholipase A2, group IVA (cytosolic)||phospholipase A2, group IVA (cytosolic, calcium-dependent)||	5321	M68874	1	1q25	Calcium-dependent cytosolic phospholipase a2; may serve to translocate Ca2+ to membrane vesicles; contains a Ca2+-dependent phospholipid-binding motif	component|cytoplasm|NR|GO:0005737|Proteome|na//cellular component|cytoplasmic vesicle|E|GO:0016023|Proteome|1904318//biological process|eicosanoid metabolism|NR|GO:0006690|Proteome|na//biological process|phospholipid metabolism|P|GO:0006644|Proteome|1904318//molecular function|calcium-dependent phospholipid binding|P|GO:0005544|Proteome|19043	subcellular localization|Cytoplasmic|NR|Proteome|1904318	selectively hydrolyzes arachidonyl phospholipids in the sn-2 position releasing arachidonic acid. together with its lysophospholipid activity, it is implicated in the 'initiation of the inflammatory response.	cytoplasmic. translocates to membrane vesicles in a calcium-dependent fashion.

||FLJ10686|| CRFG||NGB|| FLJ10690||G TP-binding protein||G protein-binding protein CRFG||	23560	NM_012341	NP_036473	10	10p15-p14	Highly similar to S. cerevisiae NOG1; may be a nucleolar G-protein	molecular function|tumor|antigen|E|GO:0008222|Proteome|30336	
||CEA||CEACAM5||CD66e|carcinoembryonic antigen-related cell adhesion molecule 5||	1048	NM_004363	NP_004354	19q13.1-19 q13.2		Carcinoembryonic antigen; member of the CEA and immunoglobulin superfamilies 6	71//cellular component|integral plasma membrane protein|P|GO: 0005887|Proteome|38146	molecular localization|Integral membrane|P| attached to the membrane by a gpi-anchor.

||MCT4||MCT 5||SLC16A4|| MCT 4||MCT 5||monocarboxylate transporter 4||MONOCARBOXYLATE TRANSPORTER 5||SOLUTE CARRIER FAMILY 16, MEMBER 4||solute carrier family 16 (monocarboxylic acid transporters), member 4||	BG752916												thyroid receptor interacting proteins (trips) specifically interact with the ligand binding domain of the thyroid receptor (tr). trip3 requires the presence of thyroid hormone for its interaction.
		||TRIP3||TRIP3||thyroid receptor interacting protein 3||thyroid hormone receptor interactor 3||	9326	AL133017		17	17q21.1	Interacts with ligand binding domain of thyroid hormone receptor	process|transcription from Pol II promoter|P|GO:0006366|Proteome|7776974	molecular function|transcription co-activator|P|GO:0003713|Proteome|7776974|biological			
		||3.4.24.16||NLN||neurotensin endopeptidase||KIAA1226 protein||neurolysin (metallopeptidase M3 family)||	57486	AB033052	NP_065777	5	5q12.3						

||ODZ1||ODZ3||TNM||TEN-M1||TNM1||tenascin M||odz (odd Oz/ten-m, Drosophila) homolog 1||odz (odd Oz/ten-m, Drosophila) homolog 3||	10178	NM_014253	NP_055068	X	Xq25	Contains an SH2 domain	process|neurogenesis|P|GO:0007399|Proteome|10341219//cellular component|extracellular|P|GO:0005576|Proteome|10341219//biological process|immune response|P|GO:0006955|Proteome|10556288//molecular function|heparin binding|P|GO:0008201|Proteome|10341219//biological process|negative control of cell proliferation|P|GO:000828	organismal role|Anti-pathogen response|E|Proteome|9771704//organismal role|Control of Cell Proliferation|P|Proteome|10556288

||IP3R2||ITPR 2||TYPE 2 INSP3 RECEPTOR|| inositol 1,4,5-triphosphate receptor, type 2||TYPE 2 INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR|| INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 2 RECEPTOR||	3709	NM_002223	NP_002214	12	12p11	Type 2 inositol 1,4,5-triphosphate receptor; may be responsible for calcium release from intracellular stores; member of a family of calcium channels	component|plasma membrane|E|GO:0005886|Proteome|10828023//biological process|signal transduction|P|GO:0007165|Proteome|8081734//cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|10828023//molecular function|calcium ion transporter|P|GO:0015085|Proteome|8081734//biological process|small molecule transport|P|G	molecular localization|Integral membrane|NR|Proteome|na//biochemical function|Receptor (signalling)|P|Proteome|8081734//biochemical function|Channel [passive transporter]|P|Proteome|8081734	receptor for inositol 1,4,5-trisphosphate, a second messenger that mediates the release of intracellular calcium.	integral membrane protein. endoplasmic reticulum.

||CS||EC 4.1.3.7||citrate synthase precursor||CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR||	1431	BC010106	NP_004068	12	12p11-qter	Citrate synthase; converts acetylCoA and oxaloacetate to citrate and CoA in TCA cycle	cellular component|mitochondrion|E|GO:0005739|Proteome|9543345//molecular function|citrate (SI)-synthase|E|GO:0004108|Proteome|9543345	biochemical function|Lyase|E|Proteome|9543345//cellular role|Energy generation|E|Proteome|9543345//subcellular localization|Mitochondrial|E|Proteome|9543345	mitochondrial matrix.
||LOC51303||FK506 binding protein precursor||	51303	NM_016594	NP_057678	12	12p11.1	Moderately similar to FKBP2; peptidyl-prolyl cis-trans isomerase			

‖COX11‖COX11P‖COX11, S. CEREVISIAE, HOMOLOG OF‖cytochrome c oxidase subunit 11, pseudogene‖CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX11, MITOCHONDRIAL PRECURSOR‖COX11 (yeast) homolog, cytochrome c oxidase assembly protein‖	1353	NM_004375	NP_004366	17 17q22	Human ortholog of yeast subunit XI of cytochrome c oxidase	process|respiration|P|GO:0007585|Proteome|9878253//cellular component|mitochondrion|E|GO:0005739|Proteome|9878253//molecular function|cytochrome-c oxidase|P|GO:0004129|Proteome|9878253//molecular function|electron transporter|P|GO:0005489|Proteome|9878253//biological process|cytochrome c oxidase biogenesis|P|GO:0008535|Proteome|98	cellular role|Energy generation|P|Proteome|9878253//biochemical function|Oxidoreductase|P|Proteome|9878253//organismal role|General cellular role|NR|Proteome|9878253//subcellular localization|Mitochondrial|E|Proteome|9878253	exerts its effect at some terminal stage of cytochrome c oxidase synthesis, probably by being involved in the insertion of the copper b into subunit i (by similarity).	mitochondrial

||LOC81537|| sphingosine-1-phosphatase|	81537	NM_030791	NP_110418	14	14q23.1

||PSC9||PSMA4||HC9||EC 3.4.25.1||PROTEASOME COMPONENT C9||PROTEASOME SUBUNIT L||MACROPAIN SUBUNIT C9||PROTEASOME SUBUNIT ALPHA TYPE 4||MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9||proteasome (prosome, macropain) subunit, alpha type, 4||	5685	AK055714	NP_002780	15	15q24.2	Alpha subunit 4 of the proteasome (prosome macropain)	cellular component|26S proteasome|E|GO:0005837|Proteome|8811196	cellular role|Protein degradation|NR|Proteome|8811196//biochemical function|Proteasome subunit|NR|Proteome|2025653	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity.	cytoplasmic and nuclear.

||DNMT3B||ICF||DNA METHYLTRANSFERASE 3B||DNA (cytosine-5-)-methyltransferase 3 beta||	1789	NM_006892	NP_008823	20	20q11.2	DNA (cytosine-5) methyltransferase 3 beta; has a role in de novo methylation of DNA	component|nucleus|P|GO:0005634|Proteome|10433969//biological process|oncogenesis|P|GO:0007048|Proteome|10325416//molecular function|DNA binding|P|GO:0003677|Proteome|10433969//biological process|DNA methylation|E|GO:0006306|Proteome|10433969//biological process|developmental processes|P|GO:0007275|Proteome|10433969//molecular function|DNA	role|Differentiation|P|Proteome|10433969//biochemical function|Transferase|P|Proteome|10433969//subcellular localization|Nuclear|P|Proteome|10433969//biochemical function|DNA-binding protein|P|Proteome|10433969//cellular role|Chromatin/chromosome structure|P|Proteome|10433969//molecular localization|DNA-associated (direct or

||IL1RB||IL-1R-BETA||IL1R2||IL-1R-2||ANTIGEN CDW121B||INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR||interleukin 1 receptor, type II||||interleukin-1 receptor, beta; type II receptor||INTERLEUKIN 1 RECEPTOR, BETA, TYPE II||	7850	NM_004633	NP_004624	2 2q12-q22	Member of the interleukin-1 receptor-like protein family; does not bind interleukin-1 (IL1) by itself	biological process|immune response|PIGO:0006955|Proteome|8898719//molecular function|interleukin-1 receptor|PIGO:0004908|Proteome|10191101	organismal role|Anti-pathogen response|NR|Proteome|8898719	receptor for interleukin-1 alpha (il-1a), beta (il-1b), and interleukin-1 receptor antagonist protein (il-1ra).	type i membrane protein.

||hypothetical protein FLJ20958||	63933	NM_022102	NP_071385	6	6p24.3-p23			
||DEXRAS1||LOC51655||AGS1||RASD1||ras-related protein||DEXAMETHASONE-INDUCED RAS PROTEIN 1||RAS PROTEIN, DEXAMETHASONE-INDUCED, 1||	51655	NM_016084	NP_057168	17	17p11.2	Activator of G-protein signaling; acts as a direct nucleotide exchange factor for Gi-Go, induced by dexamethasone; member of the Ras superfamily of small GTPases	function|GTPase|P|GO:0003924|Proteome|10471929//biological process|signal transduction|P|GO:0007165|Proteome|10673050//biological process|cell growth and maintenance|P|GO:0008151|Proteome|10673050//molecular function|guanyl-nucleotide exchange factor|NR|GO:0005085|Proteome|na//biological process|G-protein linked receptor protein signalling	biochemical function|Hydrolase|P|Proteome|10471929//biochemical function|GTP-binding protein/GTPase|P|Proteome|10471929//organismal role|Extracellular matrix maintenance|P|Proteome|10673050//biochemical function|Guanine nucleotide exchange factor|NR|Proteome|10840027

						biological process|neurogenesis|P|GO:0007399|P roteome|103 80929//biological process|cell adhesion|P|GO:0007155|P roteome|103 80929//molecular function|cell adhesion|P|GO:0005194|P roteome|103 80929//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|103809 29
||PCDH-BETA2||PCDH-BETA-2||PCDHB2|| PROTOCADHERIN-BETA 2||protocadherin beta 2 precursor||	56133	NM_018936	NP_061759	5 5q31	Member of a family of neural cadherin-like cell adhesion proteins; may have a role in forming neuronal connections in the brain	organismal|Neuronal development|P|Proteome|10 chemical|Adhesion|Proteome|10 anismal|CNS-specific functions|NR|Proteome|10 cular potential|calcium-dependent cell-adhesion protein. type i membrane protein (by similarity).

Highly similar to FLVCR, which may transport organic anions; member of the major facilitator family of transporters	14 14q24.2	NP_060261	NM_017791	55640	||hypothetical protein FLJ20371||	

||GSPT1||ERF3A||GST1||ETF3A||GTP-BINDING PROTEIN GST1-HS||G1-TO-S PHASE TRANSITION 1||GST1, YEAST, HOMOLOG OF||G1 to S phase transition 1||G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG||	2935	NM_002094	NP_002085	16	16p13.1	GTP-binding protein; has GTP-binding activity, may have a role in G1 to S phase transition; similar to polypeptide chain elongation factor EF1 alpha (EEF1A1)	molecular function|GTPase|P|GO:0003924|Proteome|2511002//biological process|cell cycle control|P|GO:0000074|Proteome|2511002//biological process|cell proliferation|P|GO:0008283|Proteome|2511002//biological process|mitotic G1/S transition|P|GO:0000082|Proteome|2511002//biological process|protein synthesis elongation|P|GO:0006414|Proteome|2511002	biochemical function|Hydrolase|P|Proteome|2511002//cellular role|Protein synthesis|P|Proteome|2511002//biochemical function|GTP-binding protein/GTPase|P|Proteome|2511002	involved in regulation of mammalian cell growth.

||AR||SDGF||AREG||CRDGF||AMPHIREGULIN PRECURSOR||COLORECTUM CELL-DERIVED GROWTH FACTOR||amphiregulin (schwannoma-derived growth factor)||	374	NM_001657	NP_001648	4	4q13-q21	Amphiregulin (schwannoma-derived growth factor); bifunctional glycoprotein; inhibits the growth of certain carcinoma cell lines but stimulates the growth of fibroblasts and epithelial cells	molecular function|growth factor|E|GO:0008083|Proteome|2466334//biological process|cell proliferation|E|GO:0008283|Proteome|2466334//cellular component|extracellular space|E|GO:0005615|Proteome|3413110//biological process|cell-cell signalling|E|GO:0007267|Proteome|2466334	molecular localization|Soluble|NR|Proteome|na//organismal role|Cell-to-cell signalling|E|Proteome|2466334//organismal role|Control of Cell Proliferation|E|Proteome|2466334//subcellular localization|Extracellular (excluding cell wall)|E|Proteome|3413110	bifunctional growth-modulating glycoprotein. inhibits growth of several human carcinoma cells in culture and stimulates proliferation of human fibroblasts and certain other tumor cells.

Weakly similar to yeast Mmt2p, which is involved in mitochondrial iron accumulation and is a member of a family of transition metal transporters	4 4p13-p12	NP_006336	NM_006345	10463	||C4orf1||HUEL||expressed in human embryonic lung||chromosome 4 open reading frame 1||	

||BPntase||3.1.3.7||BPNT1||bisphosphate 3'-nucleotidase||BISPHOSPHATE 3-PRIME-NUCLEOTIDASE||3-PRIME(2-PRIME),5-PRIME-@BISPHOSPHATE NUCLEOTIDASE 1||3'(2'),5'-bisphosphate nucleotidase 1||	10380	NM_006085	NP_006076	1 1q42.12	3'(2'), 5'-bisphosphate nucleotidase; has a role in nucleotide metabolism; in metal-dependent, lithium-inhibited phosphomonoesterases family	biological process|neurogenesis|P|GO:0007399|Proteome|10224133//molecular function|3'(2'),5'-bisphosphate nucleotidase|E|GO:0008441|Proteome|10224133//biological process|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|E|GO:0006139|Proteome|10224133	biochemical function|Hydrolase|E|Proteome|10224133//biochemical function|Other phosphatase|E|Proteome|10224133//organismal role|CNS-specific functions|P|Proteome|10224133

SULFURYLASE||SK2||PAPSS2||SAT||ATPSK2||ADENYLYLSULFATE 3'-PHOSPHOTRANSFERASE||SULFATE ADENYLYLTRANSFERASE||ADENYLYLSULFATE KINASE||SK2||3'-PHOSPHOADENOSINE-5'-PHOSPHOSULFATE SYNTHETASE||PAPSS2||EC 2.7.1.25||EC 2.7.7.4||ADENOSINE-5'-PHOSPHOSULFATE 3'-PHOSPHOTRANSFERASE||SEMD,	9060	AF074331	NP_004661	10	10q23-q24	Bifunctional polypeptide; has ATP sulfurylase and adenosine 5'-phosphosulfate kinase activites, required for the synthesis of sulfonate donor 3'-phosphoadenosine 5'-phosphosulfate	biological process|skeletal development|GO:0001501|Proteome|9771|Proteome|39|Proteome|9771708	biochemical function|Transferase|NR|Pmical function|Other gical process|nucleobase, nucleoside, nucleotide and nucleic acid metabolism|NR|Pr kinase|NR|Proteome|9771 1708//biochemical 1708//organismal role|Bone Development and Maintenance| (paps: activated sulfate donor	enzyme with both atp sulfurylase and aps kinase activity, which mediates two steps in the sulfate activation pathway. the first step is the transfer of a sulfate group to atp to yield adenosine 5'-phosphosulfate (aps), and the second step is the transfer of a phosphate group from atp to aps yielding 3'-phosphoadenosine-5'-phosphosulfate

9	6	6 6p21	NP_005856	NM_005865	10279	||TSSP||PRS S16||proteas e, serine, 16 (thymus)||thy mus specific serine peptidase||		
9	6		NP_057116	AL161962	51114	||LOC51114|| CGI-89 protein||		

‖PAELR‖ETBR-LP-1‖hET(B)R-LP‖EDNRBL‖GPR37‖ENDOTHELIN B RECEPTOR-LIKE PROTEIN-1‖PARKIN-ASSOCIATED ENDOTHELIN RECEPTOR-LIKE RECEPTOR‖PROBABLE G PROTEIN-COUPLED RECEPTOR GPR37 PRECURSOR‖G protein-coupled receptor 37 (endothelin receptor type B-like)‖	2861	U87460	NP_005293	7	7q31	Member of the G protein-coupled receptor family; has similarity to endothelin type B receptor	molecular function|G-protein linked receptor|P|GO:0004930|Proteome|9144577//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9144577//biological process|G-protein linked receptor protein signalling pathway|P|GO:0007186|Proteome|9144577	molecular localization|Integral membrane|P|Proteome|9144577//biochemical function|Receptor (signalling)|P|Proteome|9144577	orphan receptor.	integral membrane protein.

||MCJ||DNAJ domain-containing||	29103	NM_013238	NP_037370	13 13q14.1	Moderately similar to S. cerevisiae Mdj2p

||OPN3||ERO||ECPN||NMO-1||opsin 3 (encephalopsin)||	23596	NM_014322	NP_055137	1	1q43	Encephalopsin; extra-retinal opsin	molecular function|G-protein linked receptor|P|GO:0004930|Proteome|10234000//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|10234000//biological process|G-protein linked receptor protein signalling pathway|P|GO:0007186|Proteome|10234000	molecular localization|Integral membrane|P|Proteome|10234000//biochemical function|Receptor (signalling)|P|Proteome|10234000

||TREM1||triggering receptor expressed on myeloid cells 1||	54210	NM_018643	NP_061113	6 6p21.1	Member of the Ig superfamily; receptor	molecular function|receptor|E|GO:0004872|Proteome|10799849//cellular component|plasma membrane|NR|GO:0005886|Proteome|na//biological process|humoral defense mechanism|E|GO:0006959|Proteome|10799849//biological process|intracellular signalling cascade|E|GO:0007242|Proteome|10799849	organismal role|Anti-pathogen response|E|Proteome|10799849//biochemical function|Receptor (signalling)|NR|Proteome|10799849

N|CASQ2BP 1|junctate|aspartyl/asparaginyl-beta-hydroxylase|humbug|HAAH|BAH|EC 1.14.11.16|peptide-aspartate beta-dioxygenase|HAAH JUNCTIN|ASPARTYL/ASPARAGINYL BETA-HYDROXYLASE|JUNCTIN isoform 1|aspartate beta-hydroxylase, isoform e|aspartate beta-hydroxylase, isoform	444	NM_032466 NP_115857	8	8q12.1	Aspartyl beta-hydroxylase; hydroxylates aspartic acid or asparagine within EGF-like domains of some proteins	transporter|P|GO:0005489|Proteome|78 21814|cellular component|endoplasmic reticulum|E|GO:0005783|P	role|Muscle action|P|Proteome|109745 62|biochemical function|Oxidoreductase|P|Proteome|78 21814	function|calicum binding|P|GO:0005509|Proteome|11007 777|biological process|muscle contraction|P|GO:0006936|Proteome|10 974562|molecular function|electron	organismal	specifically hydroxylates an asp or asn residue in certain epidermal growth factor-like (egf) domains of a number of proteins.	type ii membrane protein. endoplasmic reticulum.

integral membrane protein. endoplasmic reticulum (by similarity).

9 9q34.2

NP_149351

NM_033161

6836

||SURF-4||SURF4||surfeit 4||SURFEIT LOCUS PROTEIN 4||

ATHIONURI A||D22S732|| GGT1||D22S 672||GGT||G GT1 DEFICIENCY ||glutamyl transpeptidas e||GAMMA- GLUTAMYLT RANSPEPTI DASE DEFICIENCY ||EC 2.3.2.2||GGT DEFICIENCY ||GTG DEFICIENCY ||gamma- glutamyltrans ferase 1 precursor||G AMMA- GLUTAMYLT RANSPEPTI DASE 1 PRECURSO R||GAMMA- GLUTAMYLT RANSFERAS E	2678	NM_013421	NP_038347	22	22q11.23	Gamma-glutamyltransferase 1; transfers g-glutamyl moiety of glutathione to an amino acid acceptor	cellular component|membrane fraction|NR|GO:0005624|Proteome|na|04146	biological process|amino acid metabolism|GO:0006520|Proteome|29|04146	cellular role|Amino-acid metabolism|Proteome|29|04146	type ii membrane protein (probable).

||L3||FLJ10243||TMSG1||SP260||LASS2||L3 pigment||tumor metastasis-suppressor||ongevity assurance (LAG1, S. cerevisiae) homolog 2||	29956	NM_013384	NP_037516	1	1q21.1

||SC5DL||SC5D||ERG3||LATHOSTEROL 5-DESATURASE||EC 1.3.3.2||Sterol C5-desaturase-like||DELTA-7-STEROL 5-DESATURASE||Lathosterol oxidase.||C-5 STEROL DESATURASE||sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)-like||ERG3, CANDIDA GLABRATA, HOMOLOG OF||	6309	NM_006918	NP_008849	11 11q23.3	Similar to S. cerevisiae Erg3p, which is a sterol-C5-desaturase	biological process||lipid metabolism||GO:0006629||Proteome||89 76377//molecular function||C-5 sterol desaturase||GO:0000248||Proteome||89 76377	biochemical function||Oxidoreductase||Proteome||89 a	catalyzes a dehydrogenation to introduce c5-6 double bond into lathosterol.	integral membrane protein. endoplasmic reticulum (probable).

||hypothetical protein FLJ22761||	80201	BC012337	NP_079406	10 10q22.3	||hypothetical protein FLJ22242||	80140	NM_025070	NP_079346	8 8p11.1			
					||SPON2||DIL-1||DIL1||spondin 2, extracellular matrix protein||	10417	NM_012445	NP_036577	4 4p16.3	Spondin 2; secreted protein	biological process|axon guidance|P|GO:0007411|Proteome|10512675//cellular component|extracellular space|NR|GO:0005615|Proteome|na	subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|10512675

||PI-PLC||P58||ERp61||ERp57||GRP57||GRP58||GRP58P||ERp60||glucose regulated protein, 58kD||ERp60 GLUCOSE-REGULATED PROTEIN, 58-KD PSEUDOGENE||	2923	NM_005313	NP_005304	15 15q15	Glucose regulated 58kDa protein; function is disputed, may act as a protease, a protein disulfide isomerase, a phospholipase, or a combination of these	5|Proteome|398923|biological process|protein-nucleus import|P|GO:0006606|Proteome|74871 4|molecular function|cysteine-type endopeptidase|E|GO:0004197|Proteome|9399589|m	process|ER retention|P|GO:0006621|Proteome|9399589|molecular function|phospholipase C|E|GO:0004629|Proteome|3398923|biological process|signal transduction|E|GO:0007165|Proteome|3398923|biological process|P|GO:0006606|Proteome|7487104|molecular function|cysteine-type endopeptidase|E|GO:0004197|Proteome|9399589|m

||transphosph oribosidase|| DHA-UROLITHIAS IS||AMP||APR T||AMP pyrophosphor ylase||AMP diphosphory| ase||EC 2.4.2.7||APR T DEFICIENCY ||adenine phosphoribos yltransferase| |APRT 2,8-@DIHYDRO XYADENINE UROLITHIAS IS||	353	NM_000485	NP_000476		16	16q24	Adenine phosphoribosyltransferase; deficiency is a cause of 2,8-dihydroxyadenine (DHA) urolithiasis	molecular function|adenine phosphoribosyltransferase| EC|GO:0003999 9|Proteome|3531209	catalyzes a salvage reaction resulting in the formation of amp, that is energically less costly than de novo synthesis.	cytoplasmic.

||TFPI-2||PP5||TFPI 2-PEN||TFPI2|| PLACENTAL PROTEIN 5||TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR||	7980	NM_006528	NP_006519	7 7q22	Member of the Kunitz-type serine protease inhibitor family; associated with the extracellular matrix, may play a role maintaining placental tissues	cellular component|extracellular matrix|E|GO:0005578|Proteome|891483 7//molecular function|serine protease inhibitor|NR| GO:0004867| Proteome|na/ /molecular function|extracellular matrix (cuticle and basement membrane)|E|GO:000520 7|Proteome|8 914837	biochemical function|Inhibitor or repressor|NR |Proteome|8914837//organismal role|Extracellular matrix maintenance| NR|Proteome |8914837//subcellular localization|E xtracellular matrix (cuticle and basement membrane)|E factor xa. has no effect on thrombin.	seems to inhibit trypsin, factor vii(a)/tissue factor, weakly secreted.

||CYCE2||CCNE2||G1/S-SPECIFIC CYCLIN E2||	9134	NM_057749	NP_477097	8	8q21.3	Cyclin E2; CDK kinase regulatory subunit that interacts with CDK2 and CDK3, functions specifically during the G1-phase of the cell cycle	biological process|oncogenesis|P|GO:0007048|Proteome|9858585//molecular function|G1/S-specific cyclin|E|GO:0003752|Proteome|9858585//biological process|cell cycle checkpoint|E|GO:0000075|Proteome|9858585//biological process|regulation of CDK activity|E|GO:0000079|Proteome|9840943	biochemical function|Regulatory subunit|E|Proteome|9858585	essential for the control of the cell cycle at the late g1 and early s phase.	nuclear.

||R-PTP-EPSILON||PTPE||PTPRE||HPTPE||EC 3.1.3.48||PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, EPSILON||PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR||protein tyrosine phosphatase, receptor type, epsilon polypeptide||	5791	NM_006504	NP_569119		10	10q26	Receptor-like protein tyrosine phosphatase	component|cytoplasm|NR|GO:0005737|Proteome|na//cellular component|soluble fraction|NR|GO:0005625|Proteome|na//biological process|protein in dephosphorylation|P|GO:0006470|Proteome|2170109//cellular component|integral membrane protein|NR|GO:0005887|Proteome|na//molecular function|transmembrane receptor protein tyrosine phosphatase|	biochemical function|Hydrolase|E|Proteome|2170109//molecular localization|Soluble|NR|Proteome|8838320//molecular localization|Cytoplasmic|NR|Proteome|8838320//molecular localization|Integral membrane|NR|Proteome|8838320//biochemical function|Receptor (signalling)|P|Proteome|2170109	type i membrane protein.

<table>
<tr><td>||SMVT||SLC5A6||SODIUM-DEPENDENT MULTIVITAMIN TRANSPORTER||NA(+)-DEPENDENT MULTIVITAMIN TRANSPORTER||SOLUTE CARRIER FAMILY 5, MEMBER 6||solute carrier family 5 (sodium-dependent vitamin transporter), member 6||</td><td>8884</td><td>NM_021095</td><td>NP_066918</td><td>2 2p23</td><td>Sodium-dependent vitamin transporter; acts in the transplacental transfer of pantothenate biotin and lipoate</td><td>cellular component|membrane fraction|P|GO:0005624|Proteome|9516450//biological process|small molecule transport|E|GO:0006832|Proteome|9516450//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9516450//molecular function|sodium dependent multivitamin transporter|E|GO:0008523|Proteome|9516450</td><td>organismal role|Progeny nutrition|E|Proteome|9516450//organismal role|Nutrient Absorption|E|Proteome|9516450//molecular localization|Integral membrane|P|Proteome|9516450//subcellular localization|Unspecified membrane|P|Proteome|9516450//biochemical function|Active transporter, secondary|E|Proteome|9516450</td></tr>
</table>

‖NAPA‖NAP1‖TA01/TA02‖ASP4‖pronapsin A‖EC 3.4.23.-‖ASP4‖NAPSIN 1 PRECURSOR‖ASPARTYL PROTEASE 4‖	9476	NM_004851	NP_004842	19	19q13.33	Pronapsin A; aspartic protease precursor	molecular function|aspartic-type endopeptidase|P|GO:0004190|Proteome|9877162//biological process|proteolysis and peptidolysis|P|GO:0006508|Proteome|9877162	biochemical function|Hydrolase|NR|Proteome|9877162//biochemical function|Protease (other than proteasomal)|NR|Proteome|9877162	may be involved in processing of pneumocyte surfactant precursors.

GP85||LIMPII||LGP85||LIMP II||CD36 ANTIGEN-LIKE 2||LYSOSOME MEMBRANE PROTEIN II||85 KDA LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN|| CD36 antigen (collagen type I receptor, thrombospondin receptor) - ||CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral	950	NM_005506	NP_005497		4	4q21.1	cellular component|membrane fraction|P|GO:0005624|Proteome|13742 38||cellular component||Lysosomal membrane protein II; a lysosomal membrane sialoglycoprotein; similar to CD36 antigen 8	Lysosomal integral membrane protein II; a lysosomal membrane sialoglycoprotein; similar to CD36 antigen 8	molecular localization|Integral membrane protein|P|GO:0005887|Proteome|137423 74238	may act as a lysosomal receptor.	type ii membrane protein. lysosomal.

||CD20-L1||MS4A4||MS4A4A||HDCME31P||membrane-spanning 4-domains, subfamily A, member 4A||	51338	NM_024021	NP_076926	11 11p11-q11		
||CRR9||DKFZP761M2324||cisplatin resistance related protein CRR9p||	81037	NM_030782	NP_110409	5 5pter-p15.3		
||LAT1-3TM protein||	81893	NM_031211	NP_112488	16 16p12	uk4	

||PDN-21||CGRP1||CT||CALC1||CCP||CGRP-I||CALCA||CALCITONIN PRECURSOR||CGRP KATACALCIN||CALCITONIN GENE-RELATED PEPTIDE||CALCITONIN CARBOXYL-TERMINAL PEPTIDE||calcitonin/calcitonin-related polypeptide, alpha||	796	NM_001741	NP_001732	11p15.2-11 p15.1	Precursor of calcitonin and calcitonin gene-related peptide; ligands for receptors found in nervous system and peripheral tissues	function|ligand|E|GO:0005102|Proteome|1761559//cellular component|soluble fraction|E|GO:0005625|Proteome|2408883//cellular component|extracellular space|E|GO:0005615|Proteome|1761559//biological process|cell-cell signalling|E|GO:0007267|Proteome|2408883//biological process|skeletal development|E|GO:0001501|Proteome|10822112//biological	molecular localization|Soluble|E|Proteome|2408883//organismal role|Cell-to-cell signalling|E|Proteome|2408883//organismal role|Bone Development and Maintenance|E|Proteome|10822112	katacalcin is a potent plasma calcium-lowering peptide.	secreted.

‖KIAA0581‖PLCB1‖phosphoinositide-specific phospholipase C-beta 1‖phospholipase C beta 1‖	23236	AB011153	NP_056007	20 20p12

||EC 1.14.11.4||LYSINE HYDROXYLASE 2||LYSYL HYDROXYLASE 2||PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE 2||PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 2 PRECURSOR||procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2||	5352	NM_000935	NP_000926	3	3q23-q24	Lysine hydroxylase; catalyzes the formation of hydroxylysine in collagens	biological process|protein modification|GO:0006464|Proteome|9054364|cellular component|endoplasmic reticulum|P|GO:0005783|Proteome|9056 4364|molecular function|proc ollagen-lysine 5-dioxygenase| GO:0008475|Proteome|9054364	biochemical function|Oxidoreductase|NR|Proteome|9054364//organismal role|Extracellular matrix maintenance| NR|Proteome|9054364	forms hydroxylysine residues in -xaa-lys-gly-sequences in collagens. these hydroxylysines serve as sites of attachment for carbohydrate units and are essential for the stability of the intermolecular collagen crosslinks.	membrane bound in cisternae of rough endoplasmic reticulum.

||TRAMP||TRAM||translocating chain-associating membrane protein||translocating chain-ssociating membrane protein||	23471	NM_014294	NP_055109	8 8q13.1	Endoplasmic reticulum membrane protein; stimulates translocation of secretory proteins	cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|1315422//cellular component|integral membrane protein|E|GO:0016021|Proteome|1315422//molecular function|endoplasmic reticulum receptor|P|GO:0005045|Proteome|1315422//biological process|co-translational membrane targeting|P|GO:0006613|Proteome|1315422	cellular role|Protein translocation|E|Proteome|1315422//molecular localization|Integral membrane|E|Proteome|1315422//biochemical function|Receptor (protein translocation)|NR|Proteome|1315422	stimulatory or required for the translocation of secretory proteins across the er membrane.	endoplasmic reticulum membrane.

||hypothetical protein FLJ22649 similar to signal peptidase SPC22/23||	60559	NM_021928	NP_068747	4 4q34.1

||LERK4||EFNA4||LERK-4||EFL4||EPLG4||EPHRIN-A4 PRECURSOR||EPHRIN A4||LIGAND OF EPH-RELATED KINASE 4||eph-related receptor tyrosine kinase ligand 4 (ephrin-A4)||	1945	NM_005227	NP_005218	1 1q21-q22	Ephrin-A4; ligand of Eph-related receptor tyrosine kinases	biological process|cell-cell signalling|P|GO:0007267|Proteome|8660976//molecular function|transmembrane-ephrin receptor|P|GO:0005005|Proteome|8660976//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|8660976	organismal role|Cell-to-cell signalling|NR|Proteome|8660976//molecular localization|Integral membrane|NR|Proteome|8660976	may play a role in the interaction between activated b lymphocytes and dendritic cells in tonsils.	attached to the membrane by a gpi-anchor or secreted (depending on the isoform).

6.1.34||EC 3.6.3.14||ATPASE SUBUNIT C||ATPASE PROTEIN 9||ATP SYNTHASE PROTEOLIPID P3||ATP synthase, mitochondrial, C subunit-3||ATP SYNTHASE LIPID-BINDING PROTEIN, MITOCHONDRIAL PRECURSOR||MITOCHONDRIAL ATP SYNTHASE, SUBUNIT C, ISOFORM 3||MITOCHONDRIAL ATP SYNTHASE, SUBUNIT 9, ISOFORM	518	NM_001689	NP_001680	2	2q31.1	Isoform 3 (P3) of subunit c, H+-translocating subunit of F0 ATP synthase; catalyzes the synthesis of ATP during oxidative phosphorylation	function|transporter|NR|GO:0005215|Proteome|na//biological process|energy pathways|NR|GO:0006091|Proteome|na//cellular component|membrane fraction|NR|GO:0005624|Proteome|na//cellular component|hydrogen-transporting ATP synthase|P|GO:0005753|Proteome|7698763//molecular function|hydrogen-transporting two-sector ATPase|P|G	function|Hydrolase|NR|Proteome|7698763//cellular role|Energy generation|NR|Proteome|7698763//subcellular localization|Mitochondrial|NR|Proteome|7698763//molecular localization|Integral membrane|NR|Proteome|7698763//subcellular localization|Unspecified membrane|NR|Proteome|7698763//biochemical function|Active transporter, primary|NR|Proteome|7698763	this protein is one of the chains of the nonenzymatic membrane component (f0) of mitochondrial atpase.	mitochondrial membrane.

||CL640||hypothetical protein||	27235	BC020728	NP_056512	1;2;11;3;17;6;12;7;5;19	Highly similar to a region of S. cerevisiae para-hydroxybenzoate-polyprenyltransferase (Coq2p), which catalyzes the second step in-the coenzyme Q (ubiquinone) biosynthesis pathway	||hypothetical protein DKFZp564D0462||	57211	AK027843	6	6q23.1-q24.3

||TP103||ADABP||DPPIV||ADCP2||DPP4||CD26||DIPEPTIDYLPEPTIDASE, INTESTINAL||EC 3.4.14.5||DPP IV||DIPEPTIDYL PEPTIDASE IV||ADENOSINE DEAMINASE COMPLEXING PROTEIN-2||T-CELL ACTIVATION ANTIGEN CD26||dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)||	1803	NM_001935	NP_001926	2	2q24.3	Dipeptidylpeptidase IV; a cell surface serine protease that interacts with adenosine deaminase (ADA)	molecular function|plasma protein|E|GO:0005209|Proteome|9710254//biological process|immune response|E|GO:0006955|Proteome|9710254//molecular function|dipeptidyl-peptidase IV|E|GO:0004274|Proteome|9710254//cellular component|peripheral plasma membrane protein|NR|GO:0000157|Proteome|na	organismal role|Pathogenic Invasion|E|Proteome|9710254//organismal role|Anti-pathogen response|E|Proteome|9710254//biochemical function|Protease (other than proteasomal)|E|Proteome|9710254	removes n-terminal dipeptides sequentially from polypeptides having unsubstituted n-termini provided that the penultimate residue is proline. plays a role in t cell activation.	type ii membrane protein. also exists in a soluble form.

component|membrane fraction|NR|GO:0005624|Proteome|na// biological process|potassium transport|E|GO:0006813|Proteome|106 92449//biological process|synaptic transmission|P|GO:0007268|Proteome|1 0692449//molecular function|potassium channel regulator|E|GO:0015459|Proteome|106 92449//cellular component|integral membrane 0792058

||KCNMB4||large-conductance calcium-activated potassium channel beta||potassium large conductance calcium-activated channel, subfamily M, beta member 4||POTASSIUM CHANNEL, CALCIUM-ACTIVATED, LARGE CONDUCTANCE, SUBFAMILY M, BETA MEMBER 4||

Beta4 subunit of the large conductance (MaxiK) Ca-activated potassium channel; regulates gating kinetics of slow K channels in a Ca-sensitive manner

27345

NM_014505

NP_055320

12 12q

||KCNS3||Kv9.3||VOLTAGE-GATED POTASSIUM CHANNEL 9.3||potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3||POTASSIUM CHANNEL, VOLTAGE-GATED, DELAYED-RECTIFIER, SUBFAMILY S, MEMBER 3||	3790	NM_002252	NP_002243	2 2p24	Voltage-gated delayed-rectifying potassium channel S3; modulates activity of potassium channel KV2.1 (KCNB1)	component|membrane fraction|NR|GO:0005624|Proteome|na//biological process|potassium transport|E|GO:0006813|Proteome|10484328//molecular function|potassium channel regulator|E|GO:0015459|Proteome|10484328//cellular component|integral plasma membrane protein|NR|GO:0005887|Proteome|na//molecular function|delayed rectifier potassium	biochemical function|Regulatory subunit|E|Proteome|10484328//molecular localization|Integral membrane|NR|Proteome|10484328//subcellular localization|Unspecified membrane|NR|Proteome|10484328

||RAB27||RAM||RAS-ASSOCIATED PROTEIN RAB-27A||GTP-BINDING PROTEIN RAM||RAS-RELATED GENE FROM MEGAKARYOCYTE||RAB 27A, member RAS oncogene family||RAB27A, member RAS oncogene family||	5873	NM_004580	NP_004571	15	15q15-q21.1	GTP-binding protein 7A; may be involved in vesicle transport; member of the RAB family of small GTPases	molecular function|RAB small monomeric GTPase|E|GO:0003928|PMID:9066979	biochemical function|Hydrolase|E|Proteome|9066979	//biochemical function|GTP-binding protein/GTPase|E|Proteome|9066979	membrane-bound.

Low similarity to Zeta crystallins; may oxidize ethanol to acetaldehyde with concomitant reduction of NAD; member of the zinc-containing alcohol dehydrogenase family	2 2p23.3	NP_004872	NM_004881	9540	‖PIG3‖quinone oxidoreductase homolog‖p53-INDUCED GENE 3‖	

OLLAGEN, TYPE IV, ALPHA-3||COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR||COLLAGEN OF BASEMENT MEMBRANE, ALPHA-3 CHAIN||collagen IV, alpha-3 polypeptide (goodpasture antigen)||collagen, type IV, alpha 3 (Goodpasture antigen)||alpha 3 type IV collagen, isoform 1, precursor||alpha 3 type IV collagen, isoform 4, precursor||alpha 3 type IV	1285	NM_000091	NP_112734	2	2q36-q37	Alpha 3 subunit of type IV collagen (Goodpasture antigen); may be an extracellular matrix protein that forms basement membranes; member of a subfamily of collagén extracellular matrix proteins	process|hearing|P|GO:0007605|Proteome|7987396//molecular function|collagen|P|GO:0005202|Proteome|7987396//biological process|circulation|E|GO:0008015|Proteome|10766752//biological process|pathogenesis|P|GO:0009405|Proteome|8016138//cellular component|collagen type IV|P|GO:0005587|Proteome|7987396//molecular function|tumor suppressor|E|GO:0008181|Proteome|10	role|Control of Cell Proliferation|E|Proteome|10837460//organismal role|Extracellular matrix component|P|Proteome|8016138//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|3025878//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|8016138//subcellular localization|Basement membrane (extracellular	type iv collagen is the major structural component of glomerular basement membranes (gbm), forming a 'chicken-wire' meshwork together with laminins, proteoglycans and entactin/nidogen.	cell surface (potential).

||PKU-ALPHA||TLK 2||serine/threonine kinase||tousled-like kinase 2||	11011	NM_006852	NP_006843	17	17q23			
||IMPA2||EC 3.1.3.25||IMP 2||IMPASE 2||inositol(myo)-1(or 4)-monophosphatase 2||MYO-INOSITOL MONOPHOSPHATASE 2||MYO-INOSITOL MONOPHOSPHATASE A2||MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 2||	3613	NM_014214	NP_055029	18	18p11.2	Putative inositol-monophosphatase 2	biological process|signal transduction|P|GO:0007165|Proteome|9322233//biological process|phosphate metabolism|P|GO:0006796|Proteome|9322233//molecular function|myo-inositol-1(or 4)-monophosphatase|P|GO:0008934|Proteome|9322233	biochemical function|Hydrolase|P|Proteome|9322233//biochemical function|Other phosphatase|P|Proteome|9322233

1||HCI||TIMP 1||EPA||CLGI||TIMP||EPO||COLLAGENASE INHIBITOR, HUMAN||FIBROBLAST COLLAGENASE INHIBITOR||METALLOPROTEINASE INHIBITOR 1 PRECURSOR|tissue inhibitor of metalloproteinase 1 precursor||Erythroid-potentiating activity (tissue inhibitor of metalloproteinases)||tissue inhibitor of metalloproteinase 1 (erythroid	7076	NM_003254	NP_003245	X	Xp11.3-p11.23	Protease inhibitor; inhibits type IV collagenase (MMP2) and stimulates growth of erythroid cells	biological process|development|processes|NR|GO:0007575|Proteome|smal|molecular function|metalloprotease inhibitor|P|GO:0008191|Proteome|750|biological process|positive control of cell proliferation|GO:0008284|Proteome|3839290	role|Photoreception|NR|Proteome|7507419|organismal role|Other|development|NR|Proteome|3839290|biochemical function|Inhibitor or repressor|NR|Proteome|03517|organismal role|Control of Cell Proliferation|NR|Proteome|3839290|ganismal role|Extracellular matrix maintenance|NR|Proteome|7507419|subcellular localization|Extracellular (excluding	with metalloproteinases (such as collagenases) and irreversibly inactivates them. also mediates erythropoiesis in vitro; but, unlike il-3, it is species-specific, stimulating the growth and differentiation of only human and murine erythroid progenitors. known to act on mmp-1, mmp-2, mmp-3, mmp-7, mmp-8, mmp-9, mmp-10, mmp-11,	secreted.

1 1p36.33	||hypothetical protein MGC3047||	84308	NM_032348	NP_115724
8 8q24.3	||hypothetical protein FLJ11856||	79581	NM_024531	NP_078807

||NRP1||NRP||VEGF165R||neuropilin 1||NEUROPILIN-1 PRECURSOR||VASCULAR ENDOTHELIAL GROWTH FACTOR-165 RECEPTOR||VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165 RECEPTOR||	8829	NM_003873	NP_003864	10 10p12	Neuropilin 1; binds to the axonal chemorepellent Semaphorin 3 and to VEGF165; member of the neuropilin protein family of receptors	process|axon guidance|E|GO:0007411|Proteome|9288753//cellular component|membrane fraction|NR|GO:0005624|Proteome|na//biological process|signal transduction|E|GO:0007165|Proteome|9288753//biological process|cell-cell signalling|E|GO:0007267|Proteome|9288753//biological process|histogenesis and organogenesis|E|GO:0007397|Proteome|9529250//bi	organismal role|Angiogenesis|E|Proteome|9529250//organismal role|Cell-to-cell signalling|E|Proteome|9288753//biochemical function|Receptor (signalling)|E|Proteome|9288753//subcellular localization|Unspecified membrane|NR|Proteome|9288753	the soluble/snrp1 isoform binds vegf-165 and appears to inhibit its binding to cells. it may also induce apoptosis by sequestering vegf-165. may bind as well various members of the semaphorin family. its expression has an averse effect on blood vessel number and integrity.	type i membrane protein. the soluble/snrp1 isoform is secreted.

||hypothetical protein FLJ22316||	80150	NM_025080	NP_079356	11 11q13.1	
||ST17||BL2||IGSF4||TSLC1||immunoglobulin superfamily, member 4||TUMOR SUPPRESSOR IN LUNG CANCER 1||	23705	AF132811	NP_055148	11 11q23.2	Low similarity to viral receptors and adhesion molecules; contains immunoglobulin (Ig) domains

||VEGF||VEGFA||VPF||VASCULAR PERMEABILITY FACTOR||VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR||	7422	NM_003376	NP_003367	6 6p12	Vascular endothelial growth factor; induces endothelial cell proliferation and vascular permeability	component|extracellular|E|GO:0005576|Proteome|9202027//biological process|stress response|E|GO:0006950|Proteome|9202027//cellular component|soluble fraction|NR|GO:0005625|Proteome|na//biological process|signal transduction|P|GO:0007165|Proteome|1711045//biological process|homophilic cell adhesion|NR|GO:0007156|Proteome|na//biological	organismal role|Angiogenesis|E|Proteome|9202027//molecular localization|Soluble|NR|Proteome|1711045	active in angiogenesis, vasculogenesis and endothelial cell growth. it induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. it binds to the vegfr1/flt-1 and vegfr2/kdr receptors and to heparan sulfate and heparin. neuropilin-1 binds isoforms vegf-	acidic and freely secreted. vegf165 is more basic, has heparin-binding properties and, although a signicant proportion remains cell-associated, most is freely secreted. vegf189 is very basic; it is cell-associated after secretion and is bound avidly by heparin and the extracellular matrix, although it may be released as a soluble form

||CAVEOLIN-1||CAV||CAV1||VIP21||caveolae protein, 22-kD||caveolin 1, beta isoform||caveolin 1, alpha isoform||caveolin 1, caveolae protein, 22kD||caveolin 1 caveolae protein, 22kD||	857	NM_001753	NP_001744	7 7q31.1	Caveolin 1; tumor suppressor and structural component of caveolar membranes, may be associated with signal transduction, endocytosis, and potocytosis	cellular component|caveolae|NR|GO:0005901|Proteome|na//molecular function|tumor suppressor|P|GO:0008181|Proteome|9801158//molecular function|structural protein|P|GO:0005198|Proteome|1360410//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|1360410	molecular localization|Integral membrane|P|Proteome|1360410	may act as a scaffolding protein within caveolar membranes. interacts directly with g-protein alpha subunits and can functionally regulate their activity (by similarity).	membrane protein of caveolae. potential hairpin-like structure in the membrane.

||ARSE||CDPX||ASE||CDPXR||CDPX1||3.1.6.1||EC 3.1.6.-||arylsulfatase E precursor||arylsulfatase E (chondrodysplasia punctata 1)||	415	NM_000047	NP_000038	X	Xp22.3	Arylsulfatase E; likely involved in warfarin embryopathy	molecular function|arylsulfatase|E|GO:0004065|Proteome|9192838//biological process|skeletal development|E|GO:0001501|Proteome|7720070	biochemical function|Hydrolase|E|Proteome|9192838//cellular role|Other metabolism|E|Proteome|9192838//organismal role|Embryonic development|P|Proteome|7720070//organismal role|Bone Development and Maintenance|E|Proteome|7720070//organismal role|Extracellular matrix maintenance|E|Proteome|7720070	may be essential for the correct composition of cartilage and bone matrix during development. has no activity toward steroid sulfates and shows maximal activity at neutral ph. is almost completely inactivated after 10 minutes at 50 degrees celsius.	golgi stack.

||TRAP-BETA||SSR2||TLAP||SSR-BETA||TRAPB||TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT PRECURSOR||SIGNAL SEQUENCE RECEPTOR BETA SUBUNIT||signal sequence receptor, beta precursor||signal sequence receptor, beta (translocon-associated protein beta)||	6746	NM_003145	NP_003136	1	1q21-q23	Signal sequence receptor beta subunit (translocon-associated protein beta); translocates newly synthesized polypeptides across the endoplasmic reticulum membrane	cellular component|endoplasmic reticulum|P|GO:0005783|Proteome|7789174//molecular function|signal sequence receptor|P|GO:0005048|Proteome|7789174//cellular component|integral membrane protein|P|GO:0016021|Proteome|7789174//biological process|co-translational membrane targeting|P|GO:0006613|Proteome|7789174	cellular role|Protein translocation|P|Proteome|7789174//molecular localization|Integral membrane|P|Proteome|7789174//biochemical function|Receptor (protein translocation)|P|Proteome|7789174	trap proteins are part of a complex whose function is to bind ca(2+) to the er membrane and thereby regulate the retention of er resident proteins.	type i membrane protein. endoplasmic reticulum.

||AIP-1||ARL6IP||KIAA0069 protein||ARL-6 INTERACTING PROTEIN-1||ADP-ribosylation factor-like 6 interacting protein||	23204	BC010281	16 16p12-p11.2	integral membrane protein (potential).

P78||BiP||MIF2||GRP78||GLUCOSE-REGULATED PROTEIN, 78-KD||HEAT-SHOCK 70-KD PROTEIN 5||IMMUNOGLOBULIN HEAVY CHAIN-BINDING PROTEIN||IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN||78 KDA GLUCOSE-REGULATED PROTEIN PRECURSOR||Heat-shock 70kD protein-5 (glucose-regulated	3309	BC020235	NP_005338	9	9q33-q34.1	Member 5 of the HSP70 family; has a role in protein folding and assembly in the ER	0249//cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|80977	biochemical function|Chaperones|NR|Proteome|80977	probably plays a role in facilitating the assembly of multimeric protein complexes inside the er.	endoplasmic reticulum lumen.	molecular function|chaperone|E|GO:0003754|Proteome|8020977 //biological process|protein in folding|E|GO:0006457|Proteome|8020977//biological process|stress response|P|GO:0006950|Proteome|284

||ARMET||AR P||arginine-rich protein||arginine-rich, mutated in early stage tumors||	7873	NM_006010	NP_006001	3 3p21.1	Arginine-rich protein	biological process|oncogenesis|PIG O:0007048|Proteome|8649854

||FGG||fibrinogen, gamma polypeptide||FIBRINOGEN--GAMMA POLYPEPTIDE CHAIN||FIBRINOGEN, G GAMMA POLYPEPTIDE||FIBRINOGEN GAMMA CHAIN PRECURSOR||fibrinogen, gamma chain, isoform gamma-B precursor||fibrinogen, gamma chain, isoform gamma-A precursor||	2266	NM_021870	NP_068656	4	4q28	Gamma subunit of fibrinogen; has a role in blood clotting and other responses to injury	function|fibrinogen|E|GO:0008001|Proteome|8470043//molecular function|cell adhesion|NR|GO:0005194|Proteome|na//biological process|blood coagulation|NR|GO:0007596|Proteome|na//cellular component|fibrinogen gamma chain|E|GO:0005974|Proteome|8470043//biological process|blood pressure regulation|NR|GO:0008217|Proteome|na//biological process|positive control of	molecular localization|Soluble|NR|Proteome|2990550//organismal role|Blood clotting|NR|Proteome|10467729//organismal role|Response to injury|NR|Proteome|10467729//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|10467729	fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

B||PO4HB||P								cellular
D||PHDB||D								componentle
S||1.14.11.2||								ndoplasmic
5.3.4.1||P4H								reticulum|P|G
B||PO4DB||E								O:0005783|P
RBA2L||GLU								roteome|303
TATHIONE-								4602//molecu
INSULIN								lar
TRANSHYD								function|prote
ROGENASE|								in disulfide
|PROCOLLA								isomerase|P|
GEN-								GO:0003756|
PROLINE,2-								Proteome|28
OXOGLUTA								46539//biolog
RATE-4-								ical
DIOXYGENA								process|prote biochemical
SE, BETA								in proline function|som
SUBUNIT||P								hydroxylation| erase|NR|Pro
ROTEIN								P|GO:000647 teome|28465
DISULFIDE								2|Proteome|2 39//biochemi
ISOMERASE					Beta subunit			of prolyl 4- 846539//mole cal
/OXIDORED					hydroxylase;			cular function|Oxid
UCTASE||PR					has protein			function|proc oreductase|N
OLYL 4-					disulfide			collagen- R|Proteome|2
HYDROXYL					isomerase			proline,2- 846539//orga
ASE, BETA					activity,			oxoglutarate- nismal
SUBUNIT||T					catalyzes			4- role|Extracell
HYROID					formation of			dioxygenase| ular matrix
HORMONE-					4-			P|GO:000465 maintenance|
BINDING					hydroxyprolin			6|Proteome|2 NR|Proteome
PROTEIN	17	17q25			e in collagens	846539		|3034602

5034

NM_000918

NP_000909

||HUMPCP||P	5547	NM_005040	NP_005031							cleaves c-
CP||PRCP||P										terminal
ROLINE										amino acids
CARBOXYP										linked to
EPTIDASE||E										proline in
C										peptides
3.4.16.2||LYS										such as
OSOMAL										angiotensin ii,
CARBOXYP						cellular				iii and des-
EPTIDASE						componently	biochemical			arg9-
C||prolylcarbo					Prolylcarboxy	sosome|NR|	function||Hydr			bradykinin.
xypeptidase					peptidase	GO:0005764|	olase|E|Prote			this cleavage
(angiotensina					(angiotensina	Proteome|na/	ome|28321//b			occurs at
se					se C); serine	/molecular	iochemical			acidic ph, but
C)||LYSOSO					carboxypepti	function|serin	function||Prot			enzymatic
MAL PRO-X					dase that	e	ease (other			activity is
CARBOXYP					removes	carboxypepti	than			retained with
EPTIDASE					residues	dase|E|GO:0	proteasomal)|			some
PRECURSO					linked to	004185|Prote	E|Proteome|2			substrates at
R||				11 11q14	proline	ome|28321	8321			neutral ph. lysosomal.

||RPN2||RPN-II||RIBIIR||ribophorin II||EC 2.4.1.119||DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR||	6185	NM_002951	NP_002942	20	20q12-q13.1	Ribophorin 2; subunit of oligosaccharyltransferase	process|protein modification|E|GO:0006464|Proteome|10660554//cellular component|endoplasmic reticulum|E|GO:0005783|Proteome|3034581//cellular component|oligosaccharyl transferase|E|GO:0008250|Proteome|10660554//molecular function|oligosaccharyl transferase|E|GO:0004576|Proteome|10660554//cellular component|endoplasmic reticulum membrane|E|	biochemical function|Transferase|NR|Proteome|10660554//molecular localization|Integral membrane|NR|Proteome|10660554	essential subunit of n-oligosaccharyl transferase. n-oligosaccharyl transferase catalyses the transfer of a high mannose oligosaccharide from a lipid-linked oligosaccharide donor onto asparagine acceptor sites within an asn-x-ser/thr consensus motif in newly synthesized proteins.	type i membrane protein. endoplasmic reticulum.

|AOC1||ABP||HISTAMINASE||ABP1||Amiloride-binding protein-1||diamine oxidase||EC 1.4.3.6||AMILORIDE-BINDING PROTEIN 1||AMILORIDE-SENSITIVE AMINE OXIDASE [COPPER-CONTAINING] PRECURSOR||amiloride binding protein 1 precursor||amiloride binding protein 1 (amine oxidase (copper-containing))||	26	NM_001091	NP_001082	7	7q34-q36	Diamine oxidase (D-amino-acid oxidase histaminase, amiloride-binding protein); deaminates putrescine and histamine	biological process|metabolism|NR|GO:0008152|Proteome|na//cellular component|peroxisome|NR|GO:0005777|Proteome|na//molecular function|amine oxidase|E|GO:0008131|Proteome|8144586//molecular function|drug binding|NR|GO:0008144|Proteome|na	cellular role|Other metabolism|E|Proteome|1356107//biochemical function|Oxidoreductase|E|Proteome|1356107//biochemical function|Small molecule-binding protein|E|Proteome|8182053	catalyzes the degradation of compounds such as putrescine, histamine, spermine, and spermidine, substances involved in allergic and immune responses, cell proliferation, tissue differentiation, tumor formation, and possibly apoptosis. placental dao is thought to play a role in the regulation of the female reproductive function.	extracellular.

||SFRSK1||SRPK1||SR protein kinase 1||SFRS protein kinase 1||PROTEIN KINASE, SERINE/ARGININE-SPECIFIC, 1||PROTEIN KINASE, ARGININE/SERINE-RICH SPLICING FACTOR, 1||	6732	NM_003137	NP_003128	6 6p21.3-p21.2	Protein kinase for Ser- and Arg-rich (SR) RNA splicing factor family; may act to control localization of splicing factors within nucleus	cellular component|nucleus|E|GO:0005634|Proteome|8208298//biological process|RNA splicing|E|GO:0008380|Proteome|8208298//molecular function|protein kinase|E|GO:0004672|Proteome|8208298//biological process|cell cycle control|P|GO:0000074|Proteome|8208298//molecular function|cell cycle regulator|P|GO:0003750|Proteome|8208298	cellular role|RNA splicing|NR|Proteome|8208298//biochemical function|Transferase|NR|Proteome|8208298//subcellular localization|Nuclear|NR|Proteome|8208298

||GPI2||PIGC||PIG-C||GPI2, YEAST, HOMOLOG OF||phosphatidylinositol glycan, class C||PHOSPHATIDYLINOSITOL-GLYCAN BIOSYNTHESIS, CLASS C PROTEIN||phosphatidylinositol glycan, class C||	5279	NM_002642	NP_002633	1	1q23-q25	Catalyzes transfer of GlcNAc to PI, required for GPI anchor synthesis	molecular function|enzyme|E|GO:0003824|Proteome|88066613// biological process|GPI anchor formation|E|GO:0006506|Proteome|8806613//cellular component|endoplasmic reticulum membrane|E|GO:0005789|Proteome|8806613	biochemical function|Transferase|NR|Proteome|88066613	involved in the first step of gpi biosynthesis. transfer of n-acetylglucosamine from udp-n-acetylglucosamine to phosphatidylinositol.	integral membrane protein. endoplasmic reticulum (potential).

||vzg-1||edg-2||EDG2||VZG1||rec.1.3||LPA RECEPTOR EDG2||ENDOTHELIAL DIFFERENTIATION GENE 2||LYSOPHOSPHATIDIC ACID RECEPTOR EDG2||VENTRICULAR ZONE GENE 1||endothelial differentiation , lysophosphatidic acid G-protein-coupled receptor, 2||	1902	NM_057159	NP_476500	9 9q32	Lysophosphatidic acid receptor; G protein-coupled receptor that activates phospholipase C; very strongly similar to murine Gpcr26	component|plasma membrane|E|GO:0005886|Proteome|9070858//molecular function|G-protein linked receptor|E|GO:0004930|Proteome|8922387//biological process|phospholipase C activation|E|GO:0007202|Proteome|9804623//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9070858//biological process|cytosolic calcium ion	molecular localization|Integral membrane|P|Proteome|9070858//biochemical function|Receptor (signalling)|E|Proteome|9070858	receptor for lysophosphatidic acid (lpa), a mediator of diverse cellular activities.	integral membrane protein.

||GLUT3P1||S						process|gluc
LC2A3P		GL						ose
UT3		GLUCO						transport|E|G
SE						O:0015758|P
TRANSPOR						roteome|169
TER 3						5905//cellular
PSEUDOGE						component|m
NE						embrane molecular
1		GLUCOSE						fraction|NR|G localization|In
TRANSPOR						O:0005624|P tegral
TER TYPE 3,						roteome|na// membrane|N
BRAIN		solut						molecular R|Proteome|1
e carrier						function|gluc 695905//subc
family 2						ose ellular
(facilitated						transporter|E| localization|U
glucose						GO:0005355| nspecified
transporter),						Proteome|16 membrane|N
member						95905//biolog R|Proteome|1
3		GLUCOSE						ical 695905//bioc
TRANSPOR						process|carb hemical
TER, FETAL						ohydrate function|Activ
SKELETAL						metabolism|N e transporter,
MUSCLE						R|GO:00059 secondary|N
SOLUTE						75|Proteome| R|Proteome|1
CARRIER						na//cellular 695905//bioc facilitative
FAMILY 2,						component|in hemical glucose
MEMBER 3						tegral function|Majo transporter.
PSEUDOGE						membrane r Facilitator probably a
NE|		6515	NM_006931	NP_008862	Facilitated	protein|NR|G Superfamily| neuronal integral
				glucose	O:0016021|P NR|Proteome glucose membrane
			12 12p13.3	transporter	roteome|na |1695905 transporter. protein.

||Bp||HP||HAPTOGLOBIN-1 PRECURSOR||HAPTOGLOBIN, BETA POLYPEPTIDE||HP HAPTOGLOBIN, ALPHA POLYPEPTIDE||	3240	AK055872	NP_005134	16	16q22.1	Haptoglobin; glycoprotein that binds free hemoglobin; similar to serine proteases	biological process|defense response|E|GO:0006952|Proteome|7036344//molecular function|plasma glycoprotein|NR|GO:0005211|Proteome|na	organismal role|Anti-pathogen response|NR|Proteome|7036344	haptoglobin combines with free plasma hemoglobin, preventing loss of iron through the kidneys and protecting the kidneys from damage by hemoglobin, while making the hemoglobin accessible to degradative enzymes.	extracellular.

3|DIF2||EX1||PRG1||EX-1||DIF-2||EX-1L|anti-death protein||PRG1|PROTEIN||DIF-2|PROTEIN||IMMEDIATE-EARLY RESPONSE GENE||IMMEDIATE-EARLY RESPONSE 3||PACAP-RESPONSIVE GENE 1|PROTEIN||DIFFERENTIATION-DEPENDENT GENE 2|PROTEIN||radiation-inducible immediate-early gene IEX-1||gly96, mouse,	8870	NM_052815	NP_434702	6 6p21.3	Differentiation-dependent (radiation-inducible immediate-early); inhibits apoptosis due to Fas or tumor necrosis factor type alpha	process|apoptosis|EIGO:0006915|Proteome|9196025//biological process|anti-apoptosis|PIGO:0006916|Proteome|9703517//molecular function|apoptosis inhibitor|EIGO:0008189|Proteome|9703517//biological process|cell growth and maintenance|EIGO:0008151|Proteome|9196025//biological process|embryonic development|Proteome|9196025//biochemical function|Inhibitor or repressor|EIProteome|9703517	type ii membrane protein (potential).

||FGB||FIBRINOGEN--BETA POLYPEPTIDE CHAIN||fibrinogen, beta chain preproprotein ||FIBRINOGEN BETA CHAIN PRECURSOR||fibrinogen, B beta polypeptide||	2244	NM_005141	NP_005132	4	4q28	Beta subunit of fibrinogen; has a role in blood clotting and other responses to injury	function|fibrinogen|P|GO:0008001|Proteome|6688356//molecular function|cell adhesion|NR|GO:0005194|Proteome|na//cellular component|soluble fraction|E|GO:0005625|Proteome|6688356//biological process|blood coagulation|NR|GO:0007596|Proteome|na//cellular component|fibrinogen beta chain|NR|GO:0005973|Proteome|na//biological process|blood pressure regulation|NR	molecular localization|Soluble|NR|Proteome|6688356//organismal role|Blood clotting|NR|Proteome|10467729//organismal role|Response to injury|NR|Proteome|10467729//subcellular localization|Extracellular (excluding cell wall)|NR|Proteome|10467729	fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

F2R||M6P-R||CD222||CI MPR||CI-MPR||MPRI||MPR 300||CI MAN-6-P RECEPTOR||MANNOSE 6-PHOSPHATE RECEPTOR, CATION-INDEPENDENT||cation-independent mannose-6 phosphate receptor||CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR||300 KDA MANNOSE 6-PHOSPHATE RECEPTOR||	3482	NM_000876	NP_000867	6	6q26	IGFII receptor/cation-independent mannose 6-phosphate receptor; binds both IGF-II and mannose 6-phosphate; putative hepatocellular tumor suppressor	function|receptor|P|GO:0004872|Proteome|7753549//molecular function|tumor suppressor|P|GO:0008181|Proteome|7753549//biological process|signal transduction|P|GO:0007165|Proteome|7753549//biological process|receptor mediated endocytosis|E|GO:0006898|Proteome|10799489//cellular component|integral plasma membrane protein|E|GO:	cellular role|Protein translocation|NR|Proteome|10799489//molecular localization|Integral membrane|NR|Proteome|10799489//biochemical function|Receptor (signalling)|NR|Proteome|7753549//biochemical function|Receptor (protein translocation)|E|Proteome|10799489	phosphorylated lysosomal enzymes from the golgi complex and the cell surface to lysosomes. lysosomal enzymes bearing phosphomannosyl residues bind specifically to mannose-6-phosphate receptors in the golgi apparatus and the resulting receptor-ligand complex is transported to an acidic prelyosomal compartment where the low ph	type i membrane protein. lysosomal.

|Niemann-Pick disease, type C1||NIEMANN-PICK C1 PROTEIN PRECURSOR||NIEMANN-PICK DISEASE, SUBACUTĖ JUVENILE FORM||NIEMANN-PICK DISEASE WITH CHOLESTEROL ESTERIFICATION BLOCK||NIEMANN-PICK DISEASE, CHRONIC NEURONOPATHIC FORM NIEMANN-PICK DISEASE C1||	4864	NM_000271	NP_000262	18	18q11-q12	Similar to the morphogen receptor PATCHED; has a role in lysosomal storage of LDL-derived cholesterol; similar to HMG-CoA reductase	component|lysosome|E|GO:0005764|Proteome|9927649//molecular function|receptor|P|GO:0004872|Proteome|9211849//cellular component|membrane fraction|P|GO:0005624|Proteome|10521290//molecular function|sterol transporter|E|GO:0015248|Proteome|9927649//molecular function|transmembrane receptor|P|GO:0004888|Proteome|10521290//cellul	organismal role|CNS-specific functions|E|Proteome|9211849//molecular localization|Integral membrane|P|Proteome|10521290//subcellular localization|Lysosome/vacuole|E|Proteome|9927649//subcellular localization|Unspecified membrane|P|Proteome|10521290	involved in the intracellular trafficking of cholesterol. may play a role in vesicular trafficking in glia, a process that may be crucial for maintaining the structural and functional integrity of nerve terminals.	integral membrane protein. found in late endosomes and lysosomes.

3||PGFS||HA								process|lipid		
KRB||KIAA01								metabolism|E		
19||3ALPHA-								|GO:0006629		
HSD||DDH1||								|Proteome|97		
AKR1C3||EC								92917//biolog		
1.3.1.20||3-								ical		
ALPHA-								process|cell		
HYDROXYS								proliferation|		
TEROID								P|GO:000828		
DEHYDROG								3|Proteome|9		
ENASE||PRO								862446//mole		
BABLE								cular		
TRANS-1,2-								function|aldo-		
DIHYDROBE								keto		
NZENE-1,2-								reductase|P|		catalyzes the
DIOL								GO:0004033|		conversion of
DEHYDROG								Proteome|97			aldehydes
ENASE||ALD								92917//molec			and ketones
O-KETO								ular			to alcohols.
REDUCTAS								function|elect			catalyzes the
E								ron	biochemical		reduction of
B||DIHYDRO					Aldo-keto			transporter|E|	function|Oxid		prostaglandin
DIOL					reductase 1,			GO:0005489|	oreductase|E|		(pg) d2, pgh2
DEHYDROG					C3 (3 alpha-			Proteome|97	Proteome|97		and
ENASE					hydroxysteroi			92917//biolog	92917//organi		phenanthren
3||PROSTAG					d			ical	smal		equinone
LANDIN F					dehydrogena			process|prost	role|Control		(pq) and the
SYNTHASE||					se); oxidizes			aglandin	of Cell		oxidation of
3-@ALPHA-					xenobiotic			metabolism|E	Proliferation|		9alpha,11bet
HYDROXYS					alicyclic			|GO:0006693	P|Proteome|9		a- pgf2 to
TEROID				10	10p15-p14	alcohols		|Proteome|97	862446		pgd2.

8644

NM_003739

NP_003730

cytoplasmic.

||RAB2||RAS-RELATED PROTEIN RAB-2||RAS-ASSOCIATED PROTEIN RAB2||RAB2, member RAS oncogene family||	5862	NM_002865	NP_002856	8 8q11.23	GTP-binding protein 2; required for vesicle transport from the ER to the Golgi complex; member of the RAB-subfamily	biological process|ER to Golgi transport|E|GO:0006888|Proteome|8910601//molecular function|RAB small monomeric GTPase|E|GO:0003928|Proteome|2501306	biochemical function|Hydrolase|E|Proteome|2501306//biochemical function|GTP-binding protein/GTPase|E|Proteome|2501306	protein transport. probably involved in vesicular traffic (by similarity).	associated with a structure having the characteristics of an intermediate compartment between the endoplasmic reticulum and the golgi apparatus.
||CCNG2||cyclin G2||	901	NM_004354	NP_004345	4 4q13.3	Cyclin G2; member of the cyclin family of CDK kinase regulatory subunits, functions specifically during the S-phase of the cell cycle	molecular function|cyclin|E|GO:0003751|Proteome|8806701//molecular function|G1/S-specific cyclin|E|GO:0003752|Proteome|8626390//biological process|cell cycle checkpoint|E|GO:0000075|Proteome|8626390	biochemical function|Regulatory subunit|NR|Proteome|8626390	may play a role in growth regulation and in negative regulation of cell cycle progesssion.	cytoplasmic (by similarity).

||PYCR1||P5C||PYCR||P5CR||Pyroline-5-carboxylate reductase-1||P5C REDUCTASE||EC 1.5.1.2||pyrroline-5-carboxylate reductase 1||PRO3, YEAST, HUMAN COMPLEMENT OF||	5831	NM_006907	NP_008838	17 17q25.3	Erythrocyte pyrroline-5-carboxylate reductase 1; reduces pyrroline-5-carboxylate to Pro in final step of Pro synthesis	biological process|proline biosynthesis|E|GO:0006561|Proteome|1730675//molecular function|pyrroline 5-carboxylate reductase|E|GO:0004735|Proteome|1730675	biochemical function|Oxidoreductase|E|Proteome|1730675//cellular role|Amino-acid metabolism|P|Proteome|1730675

||MAC-2-BP||MAC2BP||90K||LGALS3BP||Mac-2-binding protein||L3 antigen||MAC2-BINDING PROTEIN||serum protein 90K||galectin 3 binding protein||lectin, galactoside-binding, soluble, 3 binding protein||	3959	NM_005567	NP_005558	17 17q25	Mac-2-binding protein; potent immune stimulator; contains a macrophage scavenger receptor cysteine-rich domain	molecular function|scavenger receptor|P|GO:0005044|Proteome|8390986//biological process|signal transduction|P|GO:0007165|Proteome|8390986//cellular component|extracellular space|E|GO:0005615|Proteome|8390986//biological process|cellular defense response|E|GO:0006968|Proteome|8034587	organismal role|Anti-pathogen response|E|Proteome|8034587//biochemical function|Receptor (signalling)|P|Proteome|8390986//subcellular localization|Extracellular (excluding cell wall)|E|Proteome|8390986

||Nip3||BNIP3 ||BCL2/adenovirus E1B 19kD-interacting protein 3||BCL2/ADENOVIRUS E1B 19-KD PROTEIN-INTERACTING PROTEIN 3||BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 3||	664	NM_004052	NP_004043	14	14q11.2-q12	Bcl2-related protein 3; binds antiapoptotic viral E1B 19 kDa protein and cellular Bcl2 protein	biological process|anti-apoptosis|E|GO:0006916|Proteome|7954800//molecular function|apoptosis inhibitor|E|GO:0008189|Proteome|7954800	organismal role|Cell death/Apoptosis|P|Proteome|7954800	apoptosis-inducing protein that binds to the adenovirus e1b 19 kda protein or to bcl-2, and which can overcome bcl-2 suppression. also can interact with bhrf1 of epstein-barr virus.	mitochondrial. coexpression with the eib 19- kda protein results in a shift in nip3 localization pattern to the nuclear envelope.

GALNT1||EC 2.4.1.41||UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE||GalNAc TRANSFERASE 1||UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 1||protein-UDP acetylgalactosaminyltransferase 1||UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	2589	NM_020474	NP_065207	18	18q12.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl transferase 1; catalyzes O-glycosylation of serine and threonine residues	biological process|O-linked glycosylation|E|GO:0006493|Proteome|9592121//molecular function|polypeptide N-acetylgalactosaminyltransferase|E|GO:0004653|Proteome|7592619	biochemical function|Transferase|E|Proteome|7592619	this protein catalyzes the initial reaction in o-linked oligosaccharide biosynthesis, the transfer of an n-acetyl-d-galactosamine residue to a serine or threonine residue on the protein receptor.	type ii membrane protein. golgi.

||COL6A3||COLLAGEN, TYPE VI, ALPHA-3||Collagen VI, alpha-3 polypeptide||COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR||collagen, type VI, alpha 3||	1293	NM_004369	NP_476508	2 2q37	Alpha 3 subunit of type VI collagen; may be involved in maintaining the structure of connective tissue; member of a family of extracellular matrix proteins	molecular function|collagen|E|GO:0005202|Proteome|8782832//cellular component|collagen type VI|E|GO:0005589|Proteome|8782832//biological process|muscle development|P|GO:0007517|Proteome|8782832	organismal role|Extracellular matrix component|NR|Proteome|8782832//organismal role|Connective Tissue Development and Maintenance|NR|Proteome|8782832//subcellular localization|Extracellular matrix (cuticle and basement membrane)|NR|Proteome|8782832	collagen vi acts as a cell-binding protein.

||EMT||OCT3||EMTh||SLC22A3||EMT ORGANIC CATION TRANSPORTER 3||SOLUTE CARRIER FAMILY 22, MEMBER 3||solute carrier family 22 (extraneuronal monoamine transporter), member 3||solute carrier family 22 (organic cation transporter), member 3||	6581	NM_021977	NP_068812		6 6q26-q27	Member of the organic cation transporter family; strongly similar to rat OCT3 (Rn.24231)	cellular component|membrane fraction|P|GO:0005624|Proteome|99335|68//biological process|organic cation transport|P|GO:0015695|P roteome|993|3568//molecular function|organic cation transporter|P|GO:0015101|Proteome|99|33568//cellular component|tegral plasma membrane protein|P|GO:0005887|Proteome|993568	molecular localization|Integral membrane|P|99|33568//subcellular localization|Unspecified membrane|P|99|33568//biochemical function|Activ e transporter, secondary|P|99|33568//biochemical function|Majo r Facilitator Superfamily|P|Proteome|9 933568

KIT|PBT|CD117|SCFR|KIT|KIT ONCOGENE|CD117 ANTIGEN|EC 2.7.1.112|PROTO-ONCOGENE TYROSINE-PROTEIN KINASE KIT|STEM CELL FACTOR RECEPTOR|MAST CELL GROWTH FACTOR RECEPTOR|MAST/STEM CELL GROWTH FACTOR RECEPTOR PRECURSOR|v-kit Hardy-Zuckerman 4 feline sarcoma viral	3815	NM_000222	NP_000213	4	4q11-q12	Tyrosine kinase receptor; binds mast cell growth factor	process|oncogenesis|NR|GO:0007048|Proteome|na//biological process|signal transduction|P|GO:000716 5|Proteome|9990072//molecular function|protein tyrosine kinase|E|GO:0004713|Prot eome|171798 5//biological process|protein dephosphorylation|NR|GO:0006470|Prot eome|na//molecular function|receptor signalling protein tyrosine kinase|E|GO:	biochemical function|Transferase|NR|Proteome|999 0072//biochemical function|Receptor signalling protein (signalling)|NR|Proteome|9990072	this is the receptor for stem cell factor (mast cell growth factor). it has a tyrosine-protein kinase activity. binding of the ligands leads to the autophosphorylation kit and its association with substrates such as phosphatidylinositol 3-kinase (pi3k).	type i membrane protein.

Xp11.23

X
NP_055550
NM_014735
9767

||KIAA0215
gene
product||

||HPN||TMPRSS1||EC 3.4.21.- ||SERINE PROTEASE HEPSIN||hepsin (transmembrane protease, serine 1)||	3249	NM_002151	NP_002142	19	19q11-q13.2	Hepsin; transmembrane serine protease	molecular function|serine-type peptidase|P|GO:0008236|Proteome|1885621//biological process|cell growth and maintenance|P|GO:0008151|Proteome|1885621//cellular component|integral plasma membrane protein|E|GO:0005887|Proteome|1885621	molecular localization|Integral membrane|E|Proteome|1885621	plays an essential role in cell growth and maintenance of cell morphology.	type ii membrane protein.

||GRP94||GP96||TRA1||ENDOPLASMIN PRECURSOR||GP96 HOMOLOG|| TUMOR REJECTION ANTIGEN 1||Tumor rejection antigen-1 (gp96)||94 KDA GLUCOSE-REGULATED PROTEIN||glucose regulated protein, 94 kDa||tumor rejection antigen (gp96) 1||STRESS-INDUCIBLE TUMOR REJECTION ANTIGEN GP96||	7184	NM_003299	NP_003290	12q24.2-12 q24.3	Adenotin, cell-surface 96 kDa glycoprotein; binds adenosine; similar to various stress-induced proteins	process|stress response|P|GO:0006950|Proteome|2377606//cellular component|plasma membrane|E|GO:0005886|Proteome|2325637//molecular function|heat shock protein|P|GO:0003773|Proteome|2377606//molecular function|plasma glycoprotein|E|GO:0005211|Proteome|2378869//molecular function|ligand binding or carrier|E|GO:0005488|Proteome|232563	cellular role|Cell stress|P|Proteome|2377606//biochemical function|Small molecule-binding protein|E|Proteome|2325637	molecular chaperone that functions in the processing and transport of secreted proteins.	endoplasmic reticulum lumen.

||LOXL2||EC 1.4.3.-||lysyl oxidase-like 2||LYSYL OXIDASE-RELATED PROTEIN WS9-14||LYSYL OXIDASE-LIKE PROTEIN 2||LYSYL OXIDASE RELATED PROTEIN 2||LYSYL OXIDASE HOMOLOG 2 PRECURSOR||	4017	NM_002318	NP_002309	8	8p21.3-p21.2	lysyl oxidase (LOX)	Member of the scavenger receptor cysteine-rich family; may have roles in senescence and cell adhesion; similar to the C-terminal portion of lysyl oxidase	biological process|aging|P|GO:0007568|Proteome|9079631// biological process|cell adhesion|P|GO:0007155|Proteome|9079631//cellular component|extracellular space|P|GO:0005615|Proteome|907963 1//biological process|protein in modification|P|GO:0006464|Proteome|9079631//molecular function|elect ron transporter|P|GO:0005489|cell Proteome|90 79631	biological process|aging|P|Proteome|90 79631//biochemical function|Oxidoreductase|P|Proteome|90 79631//subcellular localization|Extracellular (excluding cell wall)|P|Proteome|9079631	extracellular (potential).

||hypothetical protein FLJ13868||	64755	NM_022744	NP_073581	16 16p11.1	||PTD004||hypothetical protein||homologous yeast-44.2 protein||	29789	NM_013341	NP_037473	22 22q13.2	Highly similar to GTP-binding proteins
					||WCRF180||hACF1||BAZ1A||DKFZP586E0518||ACF1||WALp1||bromodomain adjacent to zinc finger domain, 1A||	11177	NM_013448	NP_038476	14 14q12-q13	May bind DNA and act as a chromatin-mediated transcriptional regulator; contains a bromodomain and a PHD-finger

P||HF||GZMA||HANUKKAH FACTOR||CTL tryptase||EC 3.4.21.78||granzyme A precursor||CYTOTOXIC T-LYMPHOCYTE PROTEINASE 1||granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)||CYTOLYTIC T CELL-AND NATURAL KILLER CELL-SPECIFIC TRYPSIN-LIKE SERINE PROTEASE||	3001	NM_006144	NP_006135		Granzyme A (Hanukah factor); serine protease	5 5q11-q12	molecular function|granzyme A|P|GO:0004277|Proteome|8288245//bioligical process|immune response|NR|GO:0006955|Proteome|na	organismal role|Cell death/Apoptosis|NR|Proteome|88245	this enzyme is necessary for target cell lysis in cell-mediated immune responses. it cleaves after lys or arg. may be involved in apoptosis.	cytoplasmic granules.

D||MRP3||ABCC3||MLP2||ABC31||EST90757||CMOAT2||MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 3||canicular multispecific organic anion transporter||ATP-BINDING CASSETTE, SUBFAMILY C, MEMBER 3||CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 2||ATP-binding cassette, sub-family C (CFTR/MRP), member	8714	NM_020038	NP_064422	17 17q22	Canalicular multispecific organic anion transporter; ABC (ATP-binding cassette) transporter	function|ATP binding|P|GO:0005524|Proteome|9813153//cellular component|membrane fraction|P|GO:0005624|Proteome|9813153//biological process|small molecule transport|P|GO:0006832|Proteome|9813153//molecular function|organic anion transporter|P|GO:0008514|Proteome|9738950//cellular component|integral plasma membrane protein|P|GO:0005887|Proteome|9813153	biochemical function|Hydrolase|P|Proteome|9813153//molecular localization|Integral membrane|P|Proteome|9813153//biochemical function|ATP-binding cassette|P|Proteome|9813153//subcellular localization|Unspecified membrane|P|Proteome|9813153//biochemical function|Active transporter, primary|P|Proteome|9813153	may act as an inducible transporter in the biliary and intestinal excretion of organic anions.	integral membrane protein.

19 19q13.1	10430	NM_032635	NP_116024	||NIFIE14||hypothetical protein MGC1936||seven transmembrane domain protein||	
5 5p15.2	54491	NM_019018	NP_061891	||FLJ11127||hypothetical protein||	

|NM23D|nm2 3-H4||EC 2.7.4.6||NDP KINASE, MITOCHON DRIAL||MET ASTASIS INHIBITION FACTOR NM23H4||NO NMETASTAT IC PROTEIN 23, HOMOLOG 4||NUCLEOS IDE DIPHOSPHA TE KINASE, MITOCHON DRIAL PRECURSO R||NONMET ASTATIC CELLS 4, PROTEIN EXPRESSED IN||non-metastatic cells 4, protein expressed in	4833	NM_005009	NP_005000	16	16p13.3	Member of the nucleoside diphosphate kinases family	0	cellular component|mitochondrion|P|GO:0005739|Proteome|99850||biological process|nucleoside metabolism|P|GO:0009116|Proteome|99850||molecular function|nucleoside-diphosphate kinase|P|GO:0004550|Proteome|909985	0	biochemical function|Transferase|Proteome|90998 50||biochemical function|Other r kinase|P|Proteome|909985	0	major role in the synthesis of nucleoside triphosphates other than atp (by similarity).	mitochondrial intermembrane space.

||FLJ20917|| MRPL24||MRP-L18||mitochondrial ribosomal protein L24||	79590	NM_024540	NP_078816	1	1q21-q22

||AK||ADK||EC 2.7.1.20||ADENOSINE 5'-PHOSPHOTRANSFERASE||adenosine kinase, isoform a||adenosine kinase, isoform b||	132	NM_006721	NP_006712	10	10cen-q24	Adenosine kinase; catalyzes conversion of adenosine to AMP	molecular function|adenosine kinase|E|GO:0004001|Proteome|9070863//biological process|ribonucleoside monophosphate biosynthesis|E|GO:0009156|Proteome|9070863	atp dependent phosphorylation of adenosine and other related nucleoside analogs to monophosphate derivatives. serves as a potential regulator of concentrations of extracellular adenosine and intracellular adenine nucleotides.

||HFARP||FIAF||ANGPTL4||PGAR||angiopoietin-like 4||FASTING-INDUCED ADIPOSE FACTOR||PPARG ANGIOPOIETIN-RELATED PROTEIN||HEPATIC FIBRINOGEN/ANGIOPOIETIN-RELATED PROTEIN||PPAR(gamma) angiopoietin related protein||PPAR(gamma) angiopoietin related gene; angiopoietin-related protein||	51129	NM_016109	NP_647475	19	19p13.3	||SECTM1||K12||K12 protein precursor||type 1a transmembrane protein||secreted and transmembrane 1 precursor||	6398	NM_003004	NP_002995	17	17q25	May have a role in hematopoiesis and/or immune processes	function|cytokine|P|GO:0005125|Proteome|9480746// biological process|oncogenesis|P|GO:0007048|Proteome|948 0746//biological process|immune response|P|GO:0006955|Proteome|948 0746//cellular component|GO:0005794|Proteome|94 80746//cellular component|GO:0005615|Proteome|948074 6//biological process|mes	subcellular localization|GO:olgi|E|Proteome|9480746// organismal role|Other development|P|Proteome|9480746//organismal role|Anti-pathogen response|P|P0746//molecular roteome|948 0746//subcellular localization|Integral membrane|E|Proteome|94 80746//subcellular localization|Extracellular xtracellular (excluding cell wall)|E|Proteome|9480746

||ARHF||RIF|| hypothetical protein FLJ20247||ras homolog gene family, member F (in filopodia)||	54509	NM_019034	NP_061907	12 12q24.31	Member of the Ras superfamily of GTP-binding proteins	

>1.1□CTCGTCTTTCTCCCGGGAACCTTGACGACGCCTTCCGCTTGGCCCTGCCTTCTGCCGC
ATCCCCGCCGCCGCGGCGCCTT□GAGGAGCAGGAGAAGACGCAGCCGGGCCGCCGCCGTTAGA
GGGGTTCCCGGCCGCCGCTCGCCCCGTCGGCCGCCACCGC□CTCCGGGGTCAGCCCTCTCTCT
GGGTCTCCGCTTTCTCCTGCCGCCAGCGCCCGCTCATCGCCGCGATGGGGCTCCTGGA□CTCG
GAGCCGGGTAGTGTCCTAAACGTAGTGTCCACGGCACTCAACGACACGGTAGAGTTCTACCGC
TGGACCTGGTCCA□TCGCAGATAAGCGTGTGGAAAATTGGCCTCTGATGCAGTCTCCTTGGCC
TACACTAAGTATAAGCACTCTTTATCTCCTG□TTTGTGTGGCTGGGTCCAAAATGGATGAAGG
ACCGAGAACCTTTTCAGATGCGTCTAGTGCTCATTATCTATAATTTTGG□GATGGTTTTGCTT
AACCTCTTTATCTTCAGAGAGTTATTCATGGGATCATATAATGCGGGATATAGCTATATTTGC
CAGA□GTGTGGATTATTCTAATAATGTTCATGAAGTCAGGATAGCTGCTGCTCTGTGGTGGTA
CTTTGTATCTAAAGGAGTTGAG□TATTTGGACACAGTGTTTTTTATTCTGAGAAAGAAAAACA
ACCAAGTTTCTTTCCTTCATGTGTATCATCACTGTACGAT□GTTTACCTTGTGGTGGATTGGA
ATTAAGTGGGTTGCAGGAGGACAAGCATTTTTTGGAGCCCAGTTGAATTCCTTTATCC□ATGT
GATTATGTACTCATACTATGGGTTAACTGCATTTGGCCCATGGATTCAGAAATATCTTTGGTG
GAAACGATACCTG□ACTATGTTGCAACTGATTCAATTCCATGTGACCATTGGGCACACGGCAC
TGTCTCTTTACACTGACTGCCCCTTCCCCAA□ATGGATGCACTGGGCTCTAATTGCCTATGCA
ATCAGCTTCATATTTC

TCTTTCTTAACTTCTACATTCGGACATACAAAG□AGCCTAAGAAACCAAAAGCTGGAAAAACA
GCCATGAATGGTATTTCAGCAAATGGTGTGAGCAAATCAGAAAAACAACTC□ATGATAGAAAA
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GCTTGGGGGTGGGGAGAAAAGACA□AATGTGCTCTATGTCCTAGTAACTCTTAGACTGAGTAA
AGTGTTAATACCATACCCAGATGTTTTATTTATGAAGTTTTT□ATTTTAAACATTTTTTTTAA
AAATTAGCCTTGATATTCTCCAGACCAAAGCAATCATTAAGTGACTTTGGGGATTCTCCC□CC
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GTCTGAATTTTAGAC□GATCACAGAAACGGTCTTTATGAATTATTTTGATAAATTACTAATTA
TCTTATCTACTGACTGAAATCAGTGGTGTTACA□TTTTCTTGTCCAAAGCTGAAAATGTGTAT
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AAAGGCAGCATTTGAATACTCCTGTTAGTAGCAGAAATATAT□TATGAAAATTAAGATTATTG
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TGTGCTGTTAGAATAT

GTTGATTTTTATCAGGCTTTCCTTGTTTTGATTTATGGCTGTTCCTGATTTTTCATATGTGG□
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ACACCTTTGTTTTGTTGCTCAGTGTGTAATGACTGAGATTTGTAAATCTTTGT□GAACATTCT
GTACTGGTTCCCAAGAGCTATTCATTCCCTGCTACCTGATTTCAGCACAATAAATATACTTCT
GCTGTGGG□AAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA□

>10.1□GAGCAGCGCGCGCAAGCAGGCCAGGGGAAGGTGGGCGCAGGTGAGGGGCCGAGGTGT
GCGCAGGACTTTAGCCGGTTGAG□AAGGATCAAGCAGGCATTTGGAGCACAGGTGTCTAGAAA
CTTTTAAGGGGCCGGTTCAAGAAGGAAAAGTTCCCTTCTGC□TGTGAAACTATTTGGCAAGAG
GCTGGAGGGCCCAATGGCTGCAAAATTGCAACCCAACATTCCCAAAGCCAAGAGTCTAG□ATG
GCGTCACCAATGACAGAACCGCATCTCAAGGGCAGTGGGGCCGTGCCTGGGAGGTGGACTGGT
TTTCACTGGCGAGC□GTCATCTTCCTACTGCTGTTCGCCCCCTTCATCGTCTACTACTTCATC
ATGGCTTGTGACCAGTACAGCTGCGCCCTGAC□CGGCCCTGTGGTGGACATCGTCACCGGACA
TGCTCGGCTCTCGGACATCTGGGCCAAGACTCCACCTATAACGAGGAAAG□CCGCCCAGCTCT
ATACCTTGTGGGTCACCTTCCAGGTGCTTCTGTACACGTCTCTCCCTGACTTCTGCCATAAGT
TTCTA□CCCGGCTACGTAGGAGGCATCCAGGAGGGGGCCGTGACTCCTGCAGGGGTTGTGAAC
AAGTATCAGATCAACGGCCTGCA□AGCCTGGCTCCTCACGCACCTGCTCTGGTTTGCAAACGC
TCATCTCCTGTCCTGGTTCTCGCCCACCATCATCTTCGACA□ACTGGATCCCACTGCTGTGGT
GCGCCAACATCCTTGGCTATGCCGTCTCCACCTTCGCCATGGTCAAGGGCTACTTCTTC□CCC
ACCAGCGCCAGAGACTGCAAATTCACAGGCAATTTCTTTTACAACTACATGATGGGCATCGAG
TTTAACCCTCGGAT□CGGGAAGTGGTTTGACTTCAAGCTGTTCTTCAATGGGCGCCCCGGGAT
CGTCGCCTGGACCCTCATCAACCTGTCCTTCG□CAGCGAAGCAGCGGGAGCTCCACAGCCATG
TGACCAATGCCATGGT
CCTGGTCAACGTCCTGCAGGCCATCTACGTGATT□GACTTCTTCTGGAACGAAACCTGGTACC
TGAAGACCATTGACATCTGCCATGACCACTTCGGGTGGTACCTGGGCTGGGG□CGACTGTGTC
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ACCCCGC□ACGCCGTGGGCGTCCTGCTGCTGGGCCTGGTGGGCTACTACATCTTCCGGGTGGC
CAACCACCAGAAGGACCTGTTCCGC□CGCACGGATGGGCGCTGCCTCATCTGGGGCAGGAAGC
CCAAGGTCATCGAGTGCTCCTACACATCCGCCGACGGGCAGAG□GCACCACAGCAAGCTGCTG
GTGTCGGGCTTCTGGGGCGTGGCCCGCCACTTCAACTACGTCGGCGACCTGATGGGCAGCC□T
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CATCCTGCTGACCCAC□CGCTGCCTCCGGGACGAGCACCGCTGCGCCAGCAAGTACGGCCGGG
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GGCCACGCTACACTCTGCCCACACTGGTGAGCAGGAGGTCTTCCCACGCCCTGTCATTAGG□C
TGCATTTACTCTTGCT
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□TCCCCTGCCTGCTCTGCAGTCGTGGGTGGGGCCCGTGCGCCGTTTCTCCTTGGTAGCGTGCA
CGGTGTTGAACTGGGACA□CTGGGGAGAAAGGGGCTTTCATGTCGTTTCCTTCCTGCTCCTGC
TGCACAGCTGCCAGGAGTGCTCTGCCTGGAGTCTGC□AGACCTCAGAGAGGTCCCAGCACTGG
CTGTGGCTTTCAGGTGTAGGCAGGTGGGCTCTGCTTCCCGATTCCCTGTGAGCG□CCCACCCT
CTCGAAAGAATTTTCTGTCTTGCCCTGTGACTGTGCAGACTCTGGCTCGAGCAACCCGGGGAA
CTTCACCCT□CAGGGGCCTCTCCACACCTTCTCCAGCGAGGAGGTCTCAGTCCCAGCCTCGGG
AGGGCACCTCCTTTTCTGTGCTTTCTT□CCCTGAGGCATTCTTCCTCATCCCTAGGGTGTTGT
GTAGAACTCTTTTTAAACTCTATGCTCCGAGTAGAGTTCATCTTT□ATATTAAACTTCCCCTG
TTCAAAAAAAAAAAAAAAAA□

>100.1□GCGCGGCCCATGGAGTCGGGGCTGCTGCGGCCGGCGCCGGTGAGCGAGGTCATCGT
CCTGCATTACAACTACACCGGCAA□GCTCCGCGGTGCGCGCTACCAGCCGGGTGCCGGCCTGC
GCGCCGACGCCGTGGTGTGCCTGGCGGTGTGCGCCTTCATCG□TGCTAGAGAATCTAGCCGTG
TTGTTGGTGCTCGGACGCCACCCGCGCTTCCACGCTCCCATGTTCCTGCTCCTGGGCAGC□CT
CACGTTGTCGGATCTGCTGGCAGGCGCCGCCTACGCCGCCAACATCCTACTGTCGGGGCCGCT
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